



QY	361	PLEKLNNVRLPPGNCNLSSALLPGNIFTVGYPYRITVTAYSGLASASSWCGFREELAPLVGP 420	Qy	336	---ELLYTWOQPGPGEPLEHVVVDWARDGDPLEKLN -WVRLLPGNLSA-LLPGNFTVGVF 388
Db	361	PLEKLNNVRLPPGNCNLSSALLPGNIFTVGYPYRITVTAYSGLASASSWCGFREELAPLVGP 420	Db	440	RDPHSILWVGWEPNPMPQGYVTEWGLGPSPASNRSNTWRMEQNGRATGFELKENTRPQL 499
QY	421	TMLRLQDAPPCTPAIANGEVPRHQLRHLTHYLCAQSQTSPSCVMNSGNQSVTLPLDL 480	Qy	389	YRITYTAVASGLASSVNGCFFRELALPYCPTLWPLDAPPGTPTAIWGEVPRHLRGH 448
Db	421	TMLRLQDAPPCTPAIANGEVPRHQLRHLTHYLCAQSQTSPSCVMNSGNQSVTLPLDL 480	Db	500	YEITVTPLYQDTMGPSONHVAYSQENAPSHAPEL HLKHIGKTWAQLEWVPEPELGKSP 558
QY	481	PNGPCCLEWVTAATIAGGCPPGTLRLHPDNTLWRKVLPGLFLUGCGLSIATSG 540	Qy	449	LTHYTICACQSTSPSYCMVNGNTQSVTLPDLPWGPCELW-----VTA 491
Db	481	PNGPCCLEWVTAATIAGGCPPGTLRLHPDNTLWRKVLPGLFLUGCGLSIATSG 540	Db	559	LTHYTIFWTNAQNQNSPSAISLNASSRQFVHLMAASQAGATNSTVTL 616
QY	541	RCYHLRKVLPPMWVWVDPANSSQCPHMEQVPEAQPLGLDPILEVEEMPPVMESS 600	Qy	492	STIAGGCPPGPTLRLHPDNTLWRKVLPGLFLUGCGLSIATSG 548
Db	541	RCYHLRKVLPPMWVWVDPANSSQCPHMEQVPEAQPLGLDPILEVEEMPPVMESS 600	Db	617	MTLTPCGS-----ELHT-----ILGLFGILLLTLCLG ---TAWLCCSPNRK 655
QY	601	QPAQATAPLDGSYEKHLRPLTPBEGLLGPPREQVLA 636	Qy	549	VLPRTWVKEVDPANSSG-----QPHMEQVP -EAPQPLDPLILEVEEMPPP --- 595
Db	601	QPAQATAPLDGSYEKHLRPLTPBEGLLGPPREQVLA 636	Db	656	--NPWNPSPVDPAHSSGWPVTIMEEDAFOQPLGUTPTKLTLYEDEKKPWPWES 712
RESULT	2		Qy	596	-----TMESSQPAQATAP-LDSGYERHFLPPIPEELGLLGP 631
		JH0329	Db	713	NSSETCGPLTLYQTVYLQGDRAVSTQPSQSG-----TSDQ --AGPDR 754
QY		granulocyte colony-stimulating factor receptor D7 precursor - human	RESULT	3	
C;Species:	Homo sapiens (man)	C;Date:	12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999	C38252	granulocyte colony-stimulating factor receptor precursor long form - human
C;Accession:	JH0329; S21608	N;Contains:	granulocyte colony-stimulating factor, long form; granulocyte colony-stim		
R;Yar森, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Son	C;Species:	Homo sapiens (man)	C;Date:	14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999	
J. Exp. Med. 172, 1559-1570, 1990	C;Accession:	C38252; A38252; A38252; A38252; A38252; S21607	C;Accession:	C38252; A38252; A38252; A38252; A38252; S21607	
A;Title:	Expression cloning of a human granulocyte colony-stimulating factor receptor: a	R;Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.	C;Accession:	C38252; A38252; A38252; A38252; A38252; S21607	
A;Reference number:	JH0329; MUIR:91079757	Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990	A;Title:	Three different mRNAs encoding human granulocyte colony-stimulating factor receptor	
A;Accession:	JH0329	A;Status:	A;Accession:	A38252; A38252; A38252; A38252; A38252; S21607	
A;Molecule type:	mRNA	A;Molecule type: mRNA	A;Accession:	C38252	
A;Cross references:	GB:X55720; PID:CAA39252.1; PID:g31699	A;Residues:	A;Cross references:	GB:X55721; PID:931696; PID:CAA39253.1; PID:g31697	
A;Experimental source:	Placenta	A;Note:	A;Cross references:	GB:M59820; GB:M38027; NID:g183048; PID:AAA63178.1; PID:g183049	
C;Keywords:	glycoprotein; transmembrane protein	R;Seto, Y.; Fukunaga, R.; Nagata, S.	A;Cross-references:	GB:M59820; GB:M38027; NID:g183048; PID:AAA63178.1; PID:g183049	
F11-24/Domain:	signal sequence #status predicted <SIG>	J; Immunol. 148, 259-266, 1992	A;Reference number:	JH0329; MUID:91079757	
F25-56/Domain:	granulocyte colony-stimulating factor receptor D7 #status predicted <EXT>	A;Title:	A;Reference number:	JH0329; MUID:91079757	
F28-653/Domain:	extracellular #status predicted <EXT>	A;Accession:	A;Accession:	A38250	
F64-783/Domain:	transmembrane #status predicted <TRA>	A;Molecule type: mRNA	A;Accession:	A38252	
F93; 128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict	F04 LW-----GKAGQFLW-----PVFVNLETQMKNPAPRLG-----PDVDF 139	A;Residues:	A;Cross references:	GB:X55721; PID:931696; PID:CAA39253.1; PID:g31697	
Query Match	8.5%	Score 298.5; DB 2; Length 783;	A;Residues:	1-660, 708-863 <FU2>	
Local Similarity	22.5%	Pred. No. 9.7e-13; Mismatches 75; Indels 227; Gaps 34;	A;Cross-references:	GB:M59818; GB:M38025; NID:g183046; PID:AAA63176.1; PID:g183047	
Thres 160; Conservative		A;Note:	A;Note:		
QY	50	I NC SWEP I G D L G A P S E L H L Q S O K Y R S N - K T Q T V A V ----- A G R S W V A I P R Q L T M S D K L 103	R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;	R;Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;	
Db	140	LICQWEGPTEILPTSLTKSFRNCQTCQTDCLVCPKGQSHCCIPKHLJLYQNM 199	J. Exp. Med. 172, 1559-1570, 1990	J. Exp. Med. 172, 1559-1570, 1990	
QY	504	I LW-----GKAGQFLW-----PVFVNLETQMKNPAPRLG-----PDVDF 139	A;Title:	A;Title:	
Db	200	G I W Q A N E A N G T S M S M P O L C L D M D V K K L E P P M L R T D P S P L A P P A G C L Q C L W E P ----- 255	A;Accession:	A;Accession:	
QY	140	S E D D P L E A T V H A P P T W P S H K V L I C O F - H Y R R C Q E A A W T L L E P E L K T I P L T P V E I Q D L E L 198	A;Molecule type: mRNA	A;Molecule type: mRNA	
Db	256	W Q P G L H I N Q K -- C E R R H K P O R G E S W A L V G P ----- L P L E A L Q Y E L 294	A;Cross references:	GB:X55721; PID:931696; PID:CAA39253.1; PID:g31697	
QY	199	-----A N G Y K V G R C R M E K E D L W G M E S P I L S F Q T P S A P K ----- D W V W S G N L C G T P G G E E 250	A;Residues:	1-660, 708-863 <LAR>	
Db	295	C G L L P A T A Y T L Q I R C I R W P L P C H W S W P S L E R T R A P Y R V L D T W ----- 341	A;Cross references:	GB:X55721; PID:931696; PID:CAA39253.1; PID:g31697	
QY	251	-----L W L W K A P G C V Q V S K Y K W V W G G E L S P T T C C C S L I P S G A E W A R V S A V N T S W E P ----- 308	A;Note:	A;Note:	
Db	342	-----W R Q -----R Q L D P R T V Q L F W K P V P L E D S G R I Q G Y - V V S W R P S G 379	R;Hanii, M.; Horai, T.; Arakawa, S.; Le, J.; Katta, V.; Rohe, M.F.	R;Hanii, M.; Horai, T.; Arakawa, S.; Le, J.; Katta, V.; Rohe, M.F.	
QY	309	-----L T N L S -----L Y C L D S A - S A P R S V A Y S S I A G S T ----- 335	A;Title:	Arch. Biochem. Biophys. 324, 344-356, 1995	
Db	380	Q G A I L P L C N T F E L S C T F H L P S E A Q E V A L V A Y N S A G T S R P T P V V F S E R G P A L T R H A M A 439	A;Reference number:	S68331; MUID:96132662	

Result No.	Score	Query	Match	Length	DB ID	Description
1	380	10.9	862	1	I12S_HUMAN	099665 homo sapien
2	328.5	9.4	874	1	I12S_MOUSE	P97378 mus musculus
3	297.5	8.5	836	1	GCSR_HUMAN	Q9P062 homo sapien
4	277	7.9	837	1	GCSR_MOUSE	P40223 mus musculus
5	250	7.1	918	1	IL6B_HUMAN	P04089 homo sapien
6	248	7.1	917	1	IL6B_MOUSE	Q0560 mus musculus
7	226.5	6.5	918	1	IL6B	P04190 rattus norvegicus
8	206.5	5.9	1097	1	LIFR_HUMAN	P42702 homo sapien
9	169.5	5.9	1092	1	LIFR_MOUSE	P42703 mus musculus
10	164.5	4.8	1711	1	PTPO_RAT	Q64612 rattus norvegicus
11	160.5	4.6	887	1	UFO_HUMAN	P30530 homo sapien
12	157.5	4.5	1705	1	PTPO_MOUSE	P70289 mus musculus
13	155.5	4.4	1270	1	MPC_MOUSE	Q70468 mus musculus
14	154.5	4.4	880	1	TYO3_MOUSE	P55144 mus musculus
15	154.5	4.4	3067	1	CAIC_MOUSE	Q60847 mus musculus
16	151	4.3	1274	1	MPC_HUMAN	Q14896 homo sapien
17	150	4.3	888	1	UFO_MOUSE	Q00993 mus musculus
18	147.5	4.2	1302	1	NRG_DRONE	P20241 drosophila
19	146	4.2	4289	1	TENX_HUMAN	P22105 homo sapien
20	144	4.1	890	1	TYO3_HUMAN	Q06418 homo sapien
21	143.5	4.1	3063	1	CAIC_HUMAN	Q9P715 homo sapien
22	142	4.1	880	1	TYO3_RAT	P55146 rattus norvegicus
23	138.5	4.0	581	1	PRLR_BOVIN	Q28172 bos taurus
24	137	3.9	1257	1	CAML_HUMAN	P32004 homo sapien
25	137	3.9	1284	1	NRCA_CHICK	P35331 gallus gallus
26	136	3.9	2944	1	CA17_HUMAN	Q02388 homo sapien
27	135	3.9	3164	1	TEGU_HSv11	P10220 herpes simplex virus
28	134.5	3.8	1162	1	LEPR_RAT	Q62959 rattus norvegicus
29	134.5	3.8	1912	1	PTPD_HUMAN	P23468 homo sapien
30	133.5	3.8	1142	1	MPP_HUMAN	Q14324 homo sapien
31	133	3.8	1266	1	NGCA_CHICK	Q03696 gallus gallus
32	133	3.8	1897	1	PTPE_HUMAN	P10586 homo sapien
33	132.5	3.8	1328	1	FINC_PLEWA	Q91289 pteropodes

Scoring\_table: BLOSUM62  
Gappen 10.0 , Gapext 0.5  
Searched: 100059 seqs, 36664827 residues  
# number of hits satisfying chosen parameters: 100059  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Lassing first 45 summaries

Database : SwissProt\_39;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID
1	380	10.9	862	1	I12S_HUMAN
2	328.5	9.4	874	1	I12S_MOUSE
3	297.5	8.5	836	1	GCSR_HUMAN
4	277	7.9	837	1	GCSR_MOUSE
5	250	7.1	918	1	IL6B_HUMAN
6	248	7.1	917	1	IL6B_MOUSE
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8	206.5	5.9	1097	1	LIFR_HUMAN
9	169.5	5.9	1092	1	LIFR_MOUSE
10	164.5	4.8	1711	1	PTPO_RAT
11	160.5	4.6	887	1	UFO_HUMAN
12	157.5	4.5	1705	1	PTPO_MOUSE
13	155.5	4.4	1270	1	MPC_MOUSE
14	154.5	4.4	880	1	TYO3_MOUSE
15	154.5	4.4	3067	1	CAIC_MOUSE
16	151	4.3	1274	1	MPC_HUMAN
17	150	4.3	888	1	UFO_MOUSE
18	147.5	4.2	1302	1	NRG_DRONE
19	146	4.2	4289	1	TENX_HUMAN
20	144	4.1	890	1	TYO3_HUMAN
21	143.5	4.1	3063	1	CAIC_HUMAN
22	142	4.1	880	1	TYO3_RAT
23	138.5	4.0	581	1	PRLR_BOVIN
24	137	3.9	1257	1	CAML_HUMAN
25	137	3.9	1284	1	NRCA_CHICK
26	136	3.9	2944	1	CA17_HUMAN
27	135	3.9	3164	1	TEGU_HSv11
28	134.5	3.8	1162	1	LEPR_RAT
29	134.5	3.8	1912	1	PTPD_HUMAN
30	133.5	3.8	1142	1	MPP_HUMAN
31	133	3.8	1266	1	NGCA_CHICK
32	133	3.8	1897	1	PTPE_HUMAN
33	132.5	3.8	1328	1	FINC_PLEWA

#### ALIGNMENTS

RESULT 1  
I12S\_HUMAN STANDARD PRT; 862 AA.  
ID I12S\_HUMAN  
AC Q99665;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-2)  
DE (IL-12R-BETA2).  
GN IL12RB2.  
OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TAXID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97098510; PubMed=943050;  
RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,  
RA Gately M.K., Gubler U.;  
RA "A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits";  
RT Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).  
RL RN [1]  
CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.  
CC -1- SUBUNIT: DIMER/OЛИGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC ---  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
CC ---  
CC EMBL; U61498; AAB36675; 1; -.  
DR PROSTE; PS01353; IBQU.  
DR MIM: 601642; -.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR001777; FN\_III.  
DR InterPro; IPR003529; Hematopo\_receptor\_L\_F2.  
DR Pfam: PF00041; fn3; 3.  
DR SM00600; FN3; 3.  
DR PROSTE; PS01353; HEMATopo\_REC\_L\_F2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
FT CHAIN 1 21  
FT DOMAIN 22 624 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 625 641 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.  
FT DOMAIN 642 862  
FT DOMAIN 224 306  
FT DOMAIN 421 508

FT DOMAIN	519	607	FIBRONECTIN TYPE-III 3.	
FT CARBOHYD	48	48	N-LINKED (GLCNAC. . .) (POTENTIAL).	DE 2) (IL-12R-BETA2).
FT CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).	GN IL12RB2.
FT CARBOHYD	166	166	N-LINKED (GLCNAC. . .) (POTENTIAL).	OS Mus musculus (Mouse).
FT CARBOHYD	195	271	N-LINKED (GLCNAC. . .) (POTENTIAL).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT CARBOHYD	271	271	N-LINKED (GLCNAC. . .) (POTENTIAL).	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
FT CARBOHYD	347	347	N-LINKED (GLCNAC. . .) (POTENTIAL).	NCBI_TaxID:10090;
FT CARBOHYD	376	376	N-LINKED (GLCNAC. . .) (POTENTIAL).	RN [1].
FT CARBOHYD	480	480	N-LINKED (GLCNAC. . .) (POTENTIAL).	RN SEQUENCE FROM N.A.
SQ SEQUENCE	862 AA;	97134 MW;	67C0E0D946B8DD58 CRC64;	RX MEDLINE=97098510; PubMed=8943050;
				RA Presky D.H.; Yang H.; Minetti L.J.; Chua A.O.; Nabavi N.; Wu C.-Y.;
				RA Gateley M.K.; Gubler U.;
				RT "A functional interluekin 12 receptor complex is composed of two beta-type cytokine receptor subunits."
				RL FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.
				CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.
				CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
				CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
				CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
				CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
				DR EMBL: U64199; AAC36676.1; -.
				DR HSSP; P40189; 180U.
				DR MGII: MGI:1210861; IL12rb2.
				DR InterPro: IPR002996; CRLA.
				DR InterPro: IPR01777; FN_III.
				DR InterPro: IPR003529; Hematopoি-roptor_L_F2.
				DR Pfam: PF00041; fn3; 4.
				DR PRINTS; PR00014; PNTPPEIII.
				DR SMART; SM00060; FN3; 3.
				DR PROSITE; PS01353; HEMATOPOI_REC_L_F2; 1.
				KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
				FT SIGNAL 1 20 OR 23 (POTENTIAL).
				FT CHAIN 21 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
				FT DOMAIN 21 EXTRACELLULAR (POTENTIAL).
				FT DOMAIN 21 639 POTENTIAL.
				FT DOMAIN 640 656 CYTOPLASMIC (POTENTIAL).
				FT DOMAIN 657 874 FIBRONECTIN TYPE-III 1.
				FT DOMAIN 137 230 FIBRONECTIN TYPE-III 2.
				FT DOMAIN 240 322 FIBRONECTIN TYPE-III 3.
				FT DOMAIN 436 523 FIBRONECTIN TYPE-III 4.
				FT DOMAIN 534 622 FIBRONECTIN TYPE-III 4.
				FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 391 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
				FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE	874 AA;	98196 MW;	582EAD21BFBD67 CRC64;	SQ SEQUENCE 874 AA;

RESULT<sup>2</sup>  
 ID I12S\_MOUSE STANDARD; PRT; 874 AA.  
 AC P9378;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 1.ITERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-

Query Match 9.4%; Score 328.5; DB 1; Length 874;  
 Best Local Similarity 23.0%; Pred. No. 1..3e-15;  
 Matches 153; Conservative 91; Mismatches 28; Indels 153; Gaps 32;

QY 39 LQCYGVGPGLDNCSWEP-----LGDLGAPSELHLSQSQKRSNSNKTQ----- 79

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## CM protein - protein search, using sw model

Run on: May 9, 2002, 06:04:33 ; Search time 50.89 Seconds  
(without alignments)  
1828.045 Million cell updates/sec

Title: US-09-692-504-1  
Perfect score: 3498  
Sequence: 1 MRGGGRGAPFWLWPLPKLALL.....FLPTPBEGLIGPPRQPQVLA 636

Scoring table: BLOSSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

[REDACTED] number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_17;\*

- 1: sp\_archea;\*
- 2: sp\_bacteria;\*
- 3: sp\_fungi;\*
- 4: sp\_human;\*
- 5: sp\_invertebrate;\*
- 6: sp\_mammal;\*
- 7: sp\_mhc;\*
- 8: sp\_organelle;\*
- 9: sp\_phage;\*
- 10: sp\_plant;\*
- 11: sp Rodent;\*
- 12: sp\_Iivirus;\*
- 13: sp\_Vertebrate;\*
- 14: sp\_unclassified;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

RESULT	1			
ID	060624	PRELIMINARY;	PRT:	636 AA.
AC	060624;			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	CLASS I CYTOKINE RECEPTOR (CRL1 PROTEIN).			
GN	WSX1 OR CRU1.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:98362921; PubMed:9600072;			
RA	Sprecher C.A., Grant F.J., Baumgartner J.W., Presneill S.R.,			
RA	Schrader S.K., Yamagawa T., Whitmore T.E., O'Hara P.J., Foster D.F.;			
RT	"Cloning and characterization of a novel class I cytokine receptor."			
RL	Biochem. Biophys. Res. Commun. 246:82-90 (1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Zhang W., Wan T., He L., Yuan Z., Cao X.;			
RT	"A novel gp130-like cytokine receptor."			
RL	Submitted: NOV-1998 to the EMBL/GenBank/DDBJ databases.			
DR	AF051004; AAC39155.1;			
DR	AF105912; AAG2090.1; -.			
DR	Intertyp.; IPR003961; FN_III.			
DR	PF00041; fn3;			
DR	SMART; SM00060; FN3; 1.			
SQ	SEQUENCE 636 AA; 69473 MW;			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	3498	100.0	636	4	060624		060624 homo sapien
2	2044	58.4	623	11	070394		070394 homo sapien
3	326.5	9.3	861	6	Q9BEG2		Q9beg2 bos taurus
4	292	8.3	971	11	070458		070458 mus musculus
5	288.5	8.2	970	11	088821		088821 mus musculus
6	241.5	6.9	918	13	09W609		09W609 gallus gallus
7	237.5	6.8	881	13	057519		057519 xenopus laevis
8	229	6.5	710	13	057520		057520 xenopus laevis
9	226	6.5	979	4	Q99650		Q99650 homo sapien
10	212	6.1	1093	11	070535		070535 rattus norvegicus
11	191	5.5	1236	4	Q9UH13		Q9uh13 homo sapien
12	191	5.5	1308	4	Q9UH14		Q9uh14 homo sapien
13	187.5	5.4	1180	4	015051		015051 homo sapien
14	180.5	5.2	1299	4	015179		015179 homo sapien
15	180	5.1	1299	4	Q92823		Q92823 homo sapien
16	173.5	5.0	1264	5	P91767		P91767 manduca sexta
17	168	4.8	1154	11	Q9QVN3		Q9qvn3 rattus sp.
18	166.5	4.8	1146	13	Q9IBY6		Q9ibv6 gallus gallus
19	166.5	4.8	1166	11	Q9QVN4		Q9qvn4 rattus sp.

Qy	1	MRRGRGAFWLMPLPKLALLPLWWLFLQRTRPGSAGPLQCYGVGPQLDINCSWEPLGDL 60	Query Match	100.0%	Score 3498;	DB 4;	Length 636;
			Best Local Similarity	100.0%	Pred. No. 4..3e-251;		
			Matches 636;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db	1	MRRGRGAFWLMPLPKLALLPLWWLFLQRTRPGSAGPLQCYGVGPQLDINCSWEPLGDL 60					

Qy	61	GAPSELHLHQSKYRSNKTQTVAAGRSWYALPREQLTMSDKLLVNGTKAQQLPMPVVF 120	Query Match	100.0%	Score 3498;	DB 4;	Length 636;
			Best Local Similarity	100.0%	Pred. No. 4..3e-251;		



QY	39	IQCYGVGPLGDLNCSWEPGLD-----LGAPSELHILQSQ-----	DR	MGI:1330819; Osmr.
Db	130	LSCIQGERGTCTWHRGRDTHYTAYTQLQNGPKNLWQKOCNDHYCDHLDGINLTP	DR	Interpro; IPRO02996; CRIA.
QY	72	-KYRSNKT-QTVAYAAGRSHWAIPREQLTMSKLVLWGTRAGQPMLPPVFVNLETQMKPW	DR	Interpro; IPRO03529; Hematopo_receptor_L_F2.
Db	190	ESLESSYTVKTAATNSLSGASSFP-FSFTLIDIV-----RPL-PPNDIRIKF-----	DR	SMART: SM00060; FN3: 2.
QY	130	APRILOPDYDSEDDPLEATWHAAPPTEWPKVLLCQFYHRRCCOPAATLLEPELKTIPLT	DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
Db	235	-VNAVD--RCTLILWR---DGLVLNRLRVPINSRWNNAVNVN--VTNAKG	DR	SEQUENCE 971 AA; 1.0:29 MW; BECAA85BB47C1E7 CRC64;
QY	190	PVEIQDLELATGYKVYGRCRMKEKEEDLWGENWSPLSFQTPPSAP---KDWV-----VSQN	DR	MD; MGI:1330819; Osmr.
Db	278	RHDLDLKDPKPTEYEFOISSKLHLYKGSNSDWSLESLRQTPEEEPGMLNWYMHQHIDNN	DR	Interpro; IPRO0041; fn3: 3.
QY	242	LCGTPGGEPEPLLWIK-----APGPCVQSYKWWF-VGGRELSPEGTTCCS--LIPS	DR	SMART: SM00060; FN3: 2.
Db	338	-RQTSFLWNKLNSLSEARGKILH-YQVTLQKVYAGGETILQNLITEHTSNTWVIFR	DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
Q	292	GAEW ARVSAWV-TSWPLNTSLVCLDSASAPRSVAVSTAGSTELVLTWOP--GP	DR	DR
Db	390	TGNWAAAVSRANSKGSSLPTRINTIDCAELLAQPVIAKS-BGMDKLMVNTWPPEKAT	DR	DR
QY	346	GEPLEHVVWDARQDPD----LEKLNWVRLLPGNLSALLPGNFTVGVPYRITAVASSSL	DR	DR
Db	449	AQVQYVVEN-RELHPAGMNPQPLGWLNSPPYRULSALISENKPIYCYEVIRVHAL-AGDQ	DR	DR
QY	402	ASASSVWGFREELAPLVGPTLWRLQDAPPGTATAWGEVPRHLGHLYTHUIC-AQS	DR	DR
Db	507	GCNSTRGNSQHKAPLSGHINAISE-ERGSVLTISWDEPAREQMGCTLHYRIYWKERDS	DR	DR
QY	459	GTPSPVC--MNVSGNTQSVTLPLPGCEWLNLTASTAGQGPGLPPIRLHIDPNTLURW	DR	DR
Db	566	NSQPOLCEIPYRISPNSHPTDSLQ-PRTYVVLMTALPAAGESDQGNEREFCL-QGKAWW	DR	DR
QY	516	KVLPSILFLWLFLLGCGLSLATSGRCYHLRKVYL-----PRVWKEVYDPDANSSGQPH	DR	DR
Db	624	STFVAPSICMAINVG-----VLSMRCFFRQKVFLLLRQPQWSKEIPLDPANSTWAKY	DR	DR
QY	571	MEQYPEAQPLGDLTLE---VEEMEP-----PP---YMESSQPAQA-T	DR	DR
Db	679	PIVEBKTOQLADRLTENWTPPEPEPEPLYNEVLCRVTPVFRPHRSWEKGQGVQGHY	DR	DR
QY	607	APLDSGYEKHLPLP-----EELGLGP	DR	DR
Db	739	SEEDTGYSASSPPPRAPTAETGQQVDLYKVLSSKG	DR	DR
<b>Result 4</b>				
O70458		PRELIMINARY; PRT; 971 AA.	DR	RESULT 5
AC	070458;	PRELIMINARY;	DR	O88821 PRELIMINARY; PRT; 970 AA.
DT	01-AUG-1998 (TREMBlrel. 07, Created)		DR	ID 088821
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)		DR	AC 088821;
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)		DR	DT 01-NOV-1998 (TREMBlrel. 08, Created)
GN	ONCOSTATIN_M SPECIFIC RECEPTOR.		DR	DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
OS	Mus musculus (Mouse), Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		DR	DE ONCOSTATIN_M RECEPTOR BETA.
OC			DR	MUSM
OX	NCBI_TAXID=10090;		DR	OS Mus musculus (Mouse).
RN	[1]		OS	HSSP; P40189; 1BQU.
RP	SEQUENCE FROM N.A.		RP	
RX	MEDLINE=8825223; PubMed=9584176;		RX	
RA	Lindberg R.A., Juan T., Welcher A.A., Sun Y., Cupples R., Guthrie B., Fletcher F.A.;		RA	
RT	"Cloning and characterization of a specific receptor for mouse oncostatin M."		RT	
RL	Mol. Cell. Biol. 18:3357-3367(1998).		RL	
EMBL	AF058805; AJC40122.1;		EMBL	
DR			DR	
			DR	



ALIGNMENT S

Prep. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMATES

Result No.	Score	Query Match	Length	DB ID	Description
1	3498	100.0	636	19 AAW33399	Alternatively spliced Human type I cytokin Human DNAX cytokin
2	3498	100.0	636	22 AAU01853	Human haematopoietic Partial human DNAX
3	3490	99.8	636	20 AAY29781	Partial human DNAX
4	3175	90.1	578	19 AAW33398	Mouse haematopoiet
5	2875	82.2	523	20 AAY29785	Mouse type I cytokin
6	2044	58.4	623	19 AAW33400	Partial mouse DNAX
7	2044	58.4	623	22 AAU01854	Mouse DNAX cytokin
8	886.5	25.3	246	20 AAY29786	Human interleukin-10
9	400	11.4	150	20 AAY29782	Cytokine receptor-like
10	380	10.9	862	18 AAW12771	Receptor-like protein
11	298.5	8.5	783	12 APU117A1	Pathological condition diagno
12	298.5	8.5	783	12 APU117A1	Pathological condition diagno

**RESULT 2**



CC	represents the specifically claimed human DCRS1; for use in the composition of the present invention.	XX	19-MAY-1997;	97WO-US08502.
CC		XX	23-MAY-1996;	96US-0653740.
SQ	Sequence 636 AA:	XX	PA (ZYMO ) ZYMOGENETICS INC.	
	Query Match 99.8%; Score 3490; DB 20; Length 636;	PA	Baumgartner JW, Foster DC, Grant FJ, Sprecher CA;	
	Best Local Similarity 99.7%; Pred. No. 8.3e-265;	PI	WPI; 1998-018509/02.	
	Matches 634; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	XX	N-PSpB; AAT94119.	
Qy	1 MRGGRGAPFWLPLPKLALLPLWLFLQRTRPQQSGAPLQCYGVPGLDINC SWPGLDL 60	XX	Haematopoietic cytokine receptor - useful for ligand detection, and pathological condition diagnosis	
Db	1 mrgggapfwlplpkallplwlflqrtrpqqsgaplcycygvpgldincswepgldl 60	PT		
Qy	61 GAPSELHLOSOKYRSNKTOTYVAAGRSWYALPREFOLTMDSKLLWYGTKAGOPQPLMPFPFY 120	XX	Claim 1; Pages 39-43; 86PP; English.	
Db	61 gapsehlqskyskrsnktqtvavagsrwaiapreglmtdskllwgxkagqplwppfv 120	PS		
Qy	121 NLETQMKPNAPRLGPDVDFSEDDPLEATVHWAAPPWPSHXYKLICOFHYRCQEAWTILE 180	XX	The present sequence is the human haematopoietic cytokine receptor zcytor1, useful for ligand detection, and pathological condition diagnosis, including cancer. Receptor agonists of the protein can be used to stimulate the proliferation and development of target cells in vitro and in vivo. The agonists can stimulate cell mediated immunity and lymphocyte proliferation, to treat infection involving immunosuppression, e.g. viral infections. They may also be used to suppress tumours, induce cytotoxicity, treat leukopenia and enhance the regeneration of the T-cell repertoire after bone marrow transplantation. Antagonists of the protein may be used to suppress the immune system, treat autoimmune diseases, including rheumatoid arthritis, multiple sclerosis and diabetes mellitus. Immune suppression caused by the antagonists can also be used to reduce rejection of tissue or organ transplants and grafts, and to treat T-cell specific leukaemias and lymphomas.	
Dl	121 nletqmknapr1gpadvdfsecdpleatvhwappwshvliwcqhyrrqeawtile 180	XX		
Qy	181 PELKTIPLTPVIEIQDLELATQKYVYGRCRMKEEIDLNGENSPILSFQTTPSSAPKDQWVSG 240	CC		
Db	181 pelktipltpviedqlelatqkyvgrcrmeekedlwgenspilsfqtppssapkdwvsg 240	CC		
Qy	241 NCCTGPGEPEPILLWKAAPGPCKVYSYKWWENVGGRELSPBEGITCCSSLISPGAEWAVSA 300	CC		
Db	241 nlcgtptgecpillwkaapgpckvysykwwenvggrelspgitccslispgaeawarsa 300	CC		
Qy	301 VNATSWEPLTNSLVCYLDASAPRSVAVSSTAGSSTELLVWQPGCPEPLEHVVDWARDGD 360	CC		
Db	301 vnatsepltnslvcyldasaprsrvavsvastagstellvwqpgcpelehvmdwardgd 360	CC		
Qy	361 PLEKLNWVRLLPQGNLSALLPGNTYCVPYRITVTAWSGLASASSWVGFREBELAPLYGP 420	XX		
Db	361 pleklnwvrllpqnlsallpgntfygvpyritvtawsagliassasswvgfrebelaplygp 420	SQ	Sequence 578 AA;	
Qy	421 TWRLODAPPCTPATIANGEVPRHQLRSHLHTYTLCAQSGETSPVCMNVSGNTQSVTLPDL 480	Query	Match 90.1%; Score 3150; DB 19;	
Db	421 tlwrigdappgtalawgeprhqleghlhtytlcaqsqgtspsvcmnvsgntqvlpdl 480	Best Local Similarity 90.9%; Pred. No. 3e-238;		
Qy	481 PWGPCELWVATASTIAQCGPPGPILTRNLKVLPGFLIGLGGLSLATASG 540	Matches	0; Mismatches 0; Indels 58; Gaps 1;	
Db	481 pwgpcelwvtestaciaggppgilrlhpantlwkvpgflifgflgqglatsg 540	Qy	1 MRGGRGAPFWLPLPKLALLPLWLFLQRTRPQQSGAPLQCYGVPGLDINC SWPGLDL 60	
Qy	541 RCHYLHRHKVLPFRWWEKVPDPANSSSGQPHMEQVPEAQAPQLGDLPTLVEEMEPVVMESS 600	Db	1 mrggrapfwlplpkallplwlflqrtrpqqsgaplgvpqglqgdp1ngd1 60	
Db	541 rchylhrhkvpfrwwwekvpdpanssseqphmeqveaqapqldipeveemepvvmess 600	Qy	61 GAPSEHHLQSOKYRSNKTQTVAVAGRSWYALPREFLMSDKLLWYGTKAGQPLMPFPFY 120	
Qy	601 QPAQATAPLDSEGYEKHFLPTPBEGLGLGPPRPQVLA 636	Db	61 gapsehlqskyskrsnktqtvavagsrwaiapreglmtdskllwgxkagqplwppfv 120	
Db	601 qpaqatapldsgyekhflptpeelgllgpprpqvia 636	Qy	121 NDETONKPNAPRLGPVDVSDDPLBATVHKAAPPWPSHVKLICOFHYRCOEANTILE 180	
Qy	181 PELKTIPLTPVIEQDLELATQKYVYGRCRMKEEIDLNGENSPILSFQTTPSSAPKDQWVSG 240	Db	121 nletqmknapr1gpadvdfsecdpleatvhwappwshvliwcqhyrrqeawtile 180	
Db	181 pelktipltpviedqlelatqkyvgrcrmeekedlwgenspilsfqtppssapkdwvsg 240	Qy	181 PELKTIPLTPVIEQDLELATQKYVYGRCRMKEEIDLNGENSPILSFQTTPSSAPKDQWVSG 240	
Qy	241 NLCTGPGEPEPILLWKAAPGPCKVYSYKWWENVGGRELSPBEGITCCSSLISPGAEWAVSA 300	Db	181 pelktipltpviedqlelatqkyvgrcrmeekedlwgenspilsfqtppssapkdwvsg 240	
Db	241 nlctgpgepepillwkapgpckvysykwwenvggrelspgitccslispgaeawarsa 300	Qy	301 VNATSWEPLTNSLVCYLDASAPRSVAVSSTAGSSTELLVWQPGCPEPLEHVVDWARDGD 360	
Qy	301 VNATSWEPLTNSLVCYLDASAPRSVAVSSTAGSSTELLVWQPGCPEPLEHVVDWARDGD 360	Db	301 vnatswepltnslvcyldasaprsrvavsslagstellevwqpgceplhvvdwardgd 360	
DE	Human haematopoietic cytokine receptor zcytor1.	Qy	421 TLWRLQDAPPCTPATIANGEVPRHQLRSHLHTYTLCAQSGETSPVCMNVSGNTQSVTLPDL 480	
XX	Human; haematopoietic cytokine receptor; zcytor1; ligand detection;	Db	361 pleklnwvrllpqnlsallpgntfygvpyritvtawsagliassasswvgfrebelaplygp 420	
KW	cancer diagnosis; agonist; antagonist.	DB	421 tlwrigdappgtalawgeprhqleghlhtytlcaqsqgtspsvcmnvsgntqvlpdl 480	
XX	Homo sapiens.	Qy	481 PWGPCELWVATASTIAQCGPPGPILTRNLKVLPGFLIGLGGLSLATASG 540	
ID	AAW33398 standard; Protein; 578 AA.	XX		
AAW33398;		AC		
	22-MAY-1998 (first entry)	XX		
	DE Human haematopoietic cytokine receptor zcytor1.	DT		
	KW Human; haematopoietic cytokine receptor; zcytor1; ligand detection;	XX		
	KW cancer diagnosis; agonist; antagonist.	XX		
	OS Homo sapiens.	OS		
	XN WO9744455-A1.	PN		
	XX 27-NOV-1997.	PD		

Db	481	ggpcelwvtastiaqggppgpiirlhpontlrvkvpqflwgflfgcslatsq	540	Qy	114	LWPPVFVNLETQMKPNAPIRGPDYDFSEDDPLEATVHAWPTWPSHLKVYLICQHYRRQE	173
Qy	541	RCYHLRKVLFRWKEVKYPDANSQSGPIMEQYPEAQPIGDLPLLEVEEMEPVMESS	600	Db	1	wppvfvnleclqmkkpraprgpdvdsedpleatvhawptwpshlkvilcqfhrrcq	60
Db	541	rcyhrlrkvlfrwwkevkypdansss-	566	Qy	174	AAWTILEPELKTIPLTPEVIEQDLELATGYKVKYGRCPMEKEEDEDLNGEWSPSILSFQTTPSAP	233
Qy	601	QPAQATAPLDSGYEKHFLPPEELGLGPPOVLA	636	Db	61	aawtilepelktpipveiqdlelatgykvygrcmekedeewspisfqppssap	120
Db	567	------gllgpprpqvia	578	Qy	234	KDWVWSGNLCTPGGBEPLLIWKAQPCVQSYKTFWVGRELSPEGTQCCSLTPSGA	293
RESULT	5			Db	121	kdvwrsqnlgtppgeeppllwkaqgpcvqsykrfwvyygrelpqitcccslipsqa	180
ID	AY29785	standard; Protein; 523 AA.		Qy	294	EWARVSANATSWEPLTNLSCVLDSDASAPRSVAVSSIAGSTELLIVWQPGPGELEHVY	353
AC	AY29785;			Db	181	ewarvsavntswepltnlsivclssapsvassiastellivtwpgpgelehvym	240
XX				Qy	354	DWARDGDPLEKLNWYVRLPPGNLSSLALPGNFTVGVPYRITYTAVASAGLASSYWRGFREE	413
DT	04-NOV-1999	(first entry)		Db	241	dwardgdpieklnwyrppnsallpgnftvgvpyritytavasagslasswvgrfree	300
XY				Qy	414	LAPLGPTLWRLQDAPPTRAIANGEVPRQLRGLTHITLCAQSGTSPSVCMNVSNTQ	473
Q		Partial human DNAX cytokine receptor subunit 1.		Db	301	laplgptlwrlqdasppg-paiawgevprqlrghlytclaqsgtspsvcmnvsntq	360
KW		DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;		Qy	474	SVTLDDLPWGCELMVATASITAGQGPPGPIIIRLHLPDNTLRWKVLPGLFLWGLFGCG	533
KW		interleukin B30; DSS1; DCRS1; IL-B30; cytokine receptor; diagnosis;		Db	361	svtlddlpwgcelmvattasiagqgppgpirlhlpdntlrwkvpqflifwgflfgcg	420
KW		inflammatory disorder; inflammatory response; innate immunity;		Qy	534	LSLATSGRCYHLRKVLPRMWWKEVYDPAANSSGCPHMEQYPEAQPLGDLPLTLEYEMEP	593
KW		morphogenetic development; immunological disorder.		Db	421	lslatsgrcyhlrkvlprmwwkevypdpansssgphmedyqeadpgdpilevemep	480
XX		Homo sapiens.		Qy	594	PPVMMESSQPAQATAPLDGSGTEKHFLPTPEEIGLLGPPRPQVLA	636
XX				Db	481	ppvmessqpaqatapldsgyekhfptpeelgqpprpvyla	523
XX				RESULT	6		
PN	W09940195-A1.			ID	AAW33400		
XX				XX	AAW33400 standard; Protein; 623 AA.		
PD	12-AUG-1999.			AC	AAW33400;		
XX				XX	AAW33400.		
PF	05-FEB-1999;	99WO-US0600.		DT	22-MAY-1998	(first entry)	
XX				XX	Mouse haematopoietic cytokine receptor zcytor1.		
PR	13-MAY-1998;	98US-0078194.		DE			
PR	06-FEB-1998;	98US-0073941.		XX			
XX				KW	Mouse: haematopoietic cytokine receptor; zcytor1; ligand detection;		
PA	(SCHE ) SCHERRING CORP.			XX	cancer diagnosis; agonist; antagonist; murine.		
XX	Kastlein RA, Mattson JD, McClanahan TK;			OS	Mus sp.		
XX				XX			
DR	WPI: 1999-527306/44.			PN	W0974455-A1.		
DR	N-PSDB: AAZ08667.			XX			
XX				PD	27-NOV-1997.		
PT	New receptor subunits useful in the treatment inflammatory disorders			XX			
PS	Disclosure; Page 10-13; 133pp; English.			PP	19-MAY-1997:	97WO-US08502.	
XX				XX	23-MAY-1996:	96US-0653740.	
CC	The present invention describes a composition (I) comprising DNAX cytokine receptor subunit I (DCRS1), protein and DNAX soluble receptor CC cytokine receptor subunit I (DCRS1) protein, which together encode a new mammalian CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30) CC proteins, or DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1 CC is useful for screening for ligands (i.e. agonists/antagonists) from CC a library of compounds, which are useful for modulating the physiology CC or development of a cell or tissue culture e.g. inflammatory responses, CC innate immunity and/or morphogenic development. (R), antibodies and CC ligands are useful for treatment of conditions especially immunological CC disorders, associated with conditions exhibiting abnormal expression of CC (R). (R) is useful as a phosphate labeling enzyme to label substrates, CC and the subunits DRS1 and DCRS1 are useful as immunogens for generating CC antibodies, or as antigens for binding antibodies. Nucleic acids CC variants from other individuals or species. The present sequence CC represents the partial human DCRS1, given in the present invention.		PA	(ZYMO ) ZYMOGENETICS INC.			
SQ	Sequence 523 AA;			XX	PA		
Query Match	82.2%	Score 2875;	DB 20;	Length 523;	PI	Baumgartner JW, Foster DC, Sprecher CA;	
Best Local Similarity	99.6%	Pred. No. 8.9e-21;			XX	Pathological condition diagnosis	
Matches 521;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;	PS	Claim 3; Pages 54-56; 86pp; English.	
XX					XX		

The present sequence is the mouse haematopoietic cytokine receptor Zcytor, useful for ligand detection, and pathological condition diagnosis, including cancer. Receptor agonists of the protein can be used to stimulate the proliferation and development of target cells *in vitro* and *in vivo*. The agonists can stimulate cell mediated immunity and lymphocyte proliferation, to treat infection involving immunosuppression, e.g. viral infections. They may also be used to suppress tumours, induce cytotoxicity, treat leukaemias and enhance the regeneration of the T-cell repertoire after bone marrow transplantation. Antagonists of the protein may be used to suppress the immune system, treat autoimmune diseases, including rheumatoid arthritis, multiple sclerosis and diabetes mellitus. Immune suppression caused by the antagonists can also be used to reduce rejection of tissue or organ transplants and grafts, and to treat T-cell specific leukaemias and lymphomas.

07-SEP-2001 (first entry)  
**Mouse type I cytokine receptor; type-I cytokine receptor; Th2; agonist; antagonist; rejection; multi-insulin-dependent diabetes; human immunodeficiency virus; allergic rhinitis; HIV.**  
**Mus musculus.**  
**Key**  
**Location/Q**

07-SEP-2001 (first entry)  
Mouse type I cytokine receptor, mtCCR.  
Mouse; type-I cytokine receptor; TCCR; Th1; Th2; agonist; antagonist; autolummnic allograft rejection; multiple sclerosis; insulin-dependent diabetes mellitus; human immunodeficiency virus; allergic rhinitis; HIV.  
*Mus musculus.*

07-SEP-2001 (first entry)  
Mouse type I cytokine receptor, mTCR.  
Mouse; type-I cytokine receptor; TCCR; T-cell differentiation; Th1; Th2; agonist; autonomic; autoimmune inflammatory disease; allograft rejection; multiple sclerosis; inflammatory bowel disease; insulin-dependent diabetes mellitus; infectious disease; human immunodeficiency virus; allergic disorder; asthma; allergic rhinitis; HIV.  
*Mus musculus.*

X2 DT X2 DP X2 KV KV KV KV KV KV X2 OS X2 FH

FT	Peptide	1..24	<i>label</i> = Signal_peptide
FT	Modified-site	10..13	<i>label</i> = N-glycosylation site
FT	Region	14..51	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Protein	23..623	<i>note</i> = "Region of homology to human erythropoletin"
FT	Region	36..49	<i>note</i> = "Cytokine receptor family signature 1"
FT	Modified-site	43..48	<i>label</i> = Mature_mtCCR
FT	Modified-site	46..49	<i>label</i> = N-myristoylation_site
FT	Modified-site	93..96	<i>note</i> = "Asn is N-glycosylated"
FT	Modified-site	102..102	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Modified-site	130..133	<i>label</i> = N-myristoylation_site
FT	Modified-site	172..175	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Modified-site	180..187	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Modified-site	202..209	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Region	211..219	<i>note</i> = "Tyrosine kinase phosphorylation site"
FT	Modified-site	235..238	<i>note</i> = "Region of homology with murine interleukin-5 receptor"
FT	Modified-site	240..245	<i>note</i> = "Casein kinase III phosphorylation site"
FT	Modified-site	271..274	<i>label</i> = Amidation-site
FT	Modified-site	272..275	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Modified-site	295..300	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Modified-site	296..299	<i>label</i> = N-myristoylation_site
FT	Modified-site	305..308	<i>note</i> = "Asn is N-glycosylated"
FT	Modified-site	321..326	<i>note</i> = "Asn is N-glycosylated"
FT	Modified-site	323..326	<i>label</i> = N-myristoylation_site
FT	Modified-site	330..335	<i>note</i> = "Casein kinase II phosphorylation site"
FT	Modified-site	380..381	<i>label</i> = N-myristoylation_site
FT	Modified-site	387..372	<i>note</i> = "Asn is N-glycosylated"
FT	Modified-site	386..371	<i>label</i> = N-myristoylation_site
FT	Modified-site	393..398	<i>note</i> = "Asn is N-glycosylated"
FT	Modified-site	461..464	<i>label</i> = N-myristoylation_site

FT Domain  
 FT 514..532 "Asn is N-glycosylated"  
 /label= Transmembrane\_domain

FT Modified-site  
 FT 516..526 "Prokaryotic membrane lipid attachment site"  
 /note="Prokaryotic membrane lipid attachment site"  
 FT Modified-site  
 FT 525..530 "Myristoylation\_site"  
 /label= N\_myristoylation\_site

FT Modified-site  
 FT 527..532 "Myristoylation\_site"  
 /label= N\_myristoylation\_site

FT Modified-site  
 FT 606..609 "Casein kinase II phosphorylation site"  
 /note="Casein kinase II phosphorylation site"  
 FT Modified-site  
 FT 615..618 "Casein kinase II phosphorylation site"  
 /note="Casein kinase II phosphorylation site"

XX WO200129070-A2.  
 PN  
 XX 26-APR-2001.  
 XX 18-OCT-2000; 2000WO-US28827.  
 XX 20-OCT-1999; 99US-0160542.  
 PA (GETH ) GENENTECH INC.  
 XX PI De Sauvage FJ, Grewal I, Gurney AL;  
 XX WPI: 2001-308474/32.  
 DR N-PSDB; AAS03263.

XX Modulating T-cell differentiation and cytokine release profiles into Th1 and Th2 subtypes, for treating immune-related diseases in mammals, by administering modulator of type I cytokine receptor (TCCR) -  
 PS Example 1; Fig 4; 126pp; English.

CC The sequence represents mouse type I cytokine receptor, mTCCR. The invention relates to methods of modulating the differentiation of T-cells into the Th2 subtype instead of the Th1 subtype, by administering a modulator of TCCR (e.g. an antagonist) to enhance, stimulate or potentiate T-cell differentiation, or using TCCR polypeptide or its agonists to prevent, inhibit or attenuate T-cell differentiation. Th1 mediated disease in mammal can be treated by administering a TCCR antagonist and Th2 diseases by administering a TCCR agonist. Th1-mediated diseases include allograft rejection and autoimmune diseases, such as allergic encephalomyelitis, multiple sclerosis, insulin dependent diabetes mellitus, autoimmune uveoretinitis, inflammatory bowel disease or autoimmune thyroid disease. Th2-mediated diseases include infectious diseases such as leishmania major, Mycobacterium leprae, candida albicans, Toxoplasma gondii, respiratory syncytial virus and human immunodeficiency virus (HIV) and allergic disorders, such as asthma, allergic rhinitis, dermatitis and vernal conjunctivitis.

XX Sequence 623 AA;

Db 189 qnlepgtqvsgrcqengyp-wgewssplfqtpfdplpedvvsgtvctsgkrail 247  
 QY 254 LWKAFGCPVCQVSYKTYFWVGRELSPEGITGCCSLIPSGAEWARYSAVNATSWEPILNLIS 313  
 Db 248 vwkdprpcvqytytwfagdttt: i:  
 /note="spgavavswyptnls 307

FT LVCLDSASAPRSVAVSSIASTGGSTELLVWQPGPPELEHVDWARODPLEXLNWVRLPPG 373  
 QY 314 308 lvclapesapcdvgssadsgpikvxtwkgrtrkpleyyrdwaaqddsidknwrtrpp 367  
 Db 308 lvclapesapcdvgssadsgpikvxtwkgrtrkpleyyrdwaaqddsidknwrtrpp 367  
 QY 374 NLSALLPQNTFVGVYRITYTAVASGLASASSYWGFREEELAPLVGPTLWRLODAPPGTP 433  
 Db 368 nistlplgefkggbyrtrtavsgglaaapswgfreelvpagavrlpdppgcp 427  
 QY 434 AIANGEVPRIOLRGHTHYTLCAQSGTSPVCMVNSGNTOSVTLPDLPNPGCDEVAST 493  
 Db 428 vrawevprqirgqathtcigrqlstcvrnsqtatipnhsqsfkilwvtst 487  
 QY 494 TAGQGPPGPTRIRLHPDPDTLRWKVLPGLFLWLGLPLLGCLSLATS--GRCYHLRKV 549  
 Db 488 vagqqppgpdsllhpdrnlrwkpalfwslwqllimgcglslastrcqarchhwrlki 547  
 QY 550 LPRWWKVKVDPANSQSGPHMEQVPEAQPLGDPLTILEVEREMEPPVMESQQAATAPL 609  
 Db 548 lpqwiwrypdpanssggpyikevs1lppkdpq1veeveelqpves--pkasap1 604  
 QY 610 DSGYKHKFLPTPEEIGL 627  
 Db 605 ysgyekhf1ptpeelg1 622

RESULT 8  
 ID AAY29786 standard; Protein: 246 AA.  
 XX AAY29786;  
 AC XX  
 DT 04-NOV-1999 (first entry)  
 XX Partial mouse DNAX cytokine receptor subunit 1.  
 DE XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 KW interleukin B30; DPS1; DCRS1; IL-B30; cytokine receptor; diagnosis;  
 KW inflammatory disorder; inflammatory response; innate immunity;  
 KW morphogenetic development; immunological disorder.  
 OS XX Mus sp.  
 PN W09940195-A1.  
 PD 12-AUG-1999.  
 XX PR 05-FEB-1999; 99WO-US02600.  
 PR 13-MAY-1998; 98US-0078194.  
 PR 06-FEB-1998; 98US-007941.  
 PA (SCHERING CORP.  
 PI Kastlein RA, Mattson JD, McClanahan TK;  
 XX DR WPI; 1999-527306/44.  
 DR N-PSDB; AAZ08868.  
 PT New receptor subunits useful in the treatment inflammatory disorders  
 XX Disclosure; Page 13-14; 133pp; English.  
 CC The present invention describes a composition (I) comprising DNAX  
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 CC subunit I (DPS1) protein, which together encode a new mammalian receptor  
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)

Query Match 58 4%; Score 2044; DB 22; Length 623;  
 Best Local Similarity 62.8%; Pred. No. 1.3e-151; Indels 8; Gaps 3;  
 Matches 388; Conservative 61; Mismatches 161;

QY 14 LPKALLPLWVLFQRTTRPQGSAGPLQCYGVGPIDLNCSWEPLGQSEJHLQSKY 73  
 Db 9 lptplllsmltgt-phgsppqplqcysvgplilncswepgdltppvlyhgsqky 68  
 QY 74 RSNEKTQTVAVAAGRWSWATPREQLTMSDKLLYWGTAKAGPLWPPFVNLETOKKPNAPL 133  
 Db 69 hpntrwvkvpsraswtipreftmklltgqtkrplussvntetqmkpdpq1 128  
 QY 134 GPDVDFSENDPLPLATVHNPPTWPSHKVYLICOHYRRQEAWTLLPELKTIPLTPVEI 193  
 Db 129 fsgvdiseatataqtwappwppqkaltqcfrykecqawtrleqplktqdtlpvem 188  
 QY 194 QDLELATGKVKYGRCRMKEEIDLGEWSPLSFQTPPSAPKDVWSGLCGPGEEBPL 253

proteins, or DRSR1 and IL-B30 proteins. (I) comprising DRSR1 and DCRS1 is useful for screening for ligands (i.e. agonists/antagonists) from a library of compounds which are useful for modulating the physiology or development of a cell or tissue culture e.g. inflammatory responses, innate immunity and/or morphogenetic development. (R), antibodies and ligands are useful for treatment of conditions, especially immunological disorders, associated with conditions exhibiting abnormal expression of (R). (R) is useful as a phospho labeling enzyme to label substrates, and the subunits DSR1 and DCRS1 are useful as immunogens for generating antibodies, or as antigens for binding antibodies. Nucleic acids encoding (R) are useful for identifying related DNAs and mRNAs, and variants from other individuals or species. The present sequence represents the partial mouse DCRS1, given in the present invention.

Query Match	25	3%	Score 886.5;	DB 20;	Length 246;
Best Local Similarity	67.1%		Pred. No. 1.5e-61;		
Chees	165;	Conservative	27;	Mismatches	47;
				Indels	7;
				Gaps	2;
Query	3865	GVPYRITVAASAGLASASSWSGFFREEAPLVQPTLWNLQDAPPGTNIAWGEVPRHQL	445		
	b	:             :             :             :             :			
	b	3 gvpvritvavsglaapswgfreelvplagpavrwlpdppgtqvawgevprqng	62		
Query	4466	RGHDTHTYLCAQSGETSPSYCMANSGNTQSVTLPUPWGCELNVASTTAGQPPGPILR	505		
	b	:           :           :           :           :			
	b	63 rqgacthytfciqsglslstcrnmsqsgtqlphsflkhvtsvaghqgppdpds	122		
Query	506	LHLPOINTLKVLKVLPGILWLGLI:LUGCGLSLATS---GRCYHLRKVLPRLWVKEVPPDP	561		
	b	:       :       :       :       :       :       :       :			
	b	123 lhlpdnrikwkpalwfslsrgllmgcgslastrclqsrchhrk1lPqwiwvrvpdp	182		

562	ANSSSGGPHMEQVEPAQPLGLDPLTILEVEEMPPVMESSQPAQTAPLDGYSYKEHFLPTP	621
183	anssnggph_kevlpqkpdgplveevlppvvv--plasaplysgekhpctp	239

Y	622 EELGLL 627
b	240 eelglL 245

RESULT 9  
AY29782  
D AAY9782 standard; Protein; 150 AA

X X AAY29782;  
C C 04-NOV-1999 (first entry)

**Mouse DNAX cytokine receptor subunit 1.**

Mus sp.	X		
	S		
	X		
		Key	Location/Qualifiers
		Misc-difference	150
			/label= unknown
			/action= "enclosed by can-

/note- enclued by GRN  
XX W09940195-A1.  
ON XX  
XX DD 12-AUG-1999.  
XX FF 05-FEB-1999;  
XX 99W0-US02600.  
XX PR 13-MAY-1998;  
XX PR 98US-0078194.  
XX PR 06-FEB-1998;  
XX 98US-0073941.

PA (SCHE ) SCHERING CORP.  
 XX Kastelein RA, Mattison  
 XX PI WPI: 1999-527306/44.  
 XX DR N-PSDB; AA208864.  
 XX PT New receptor subunits  
 XX PS Claim 2: Page 17-18; 1  
 XX CC The present invention  
 CC cytokine receptor subunit I (DSRSI) and/or  
 CC cytokine receptor subunit II (DSRSII) receptor  
 CC proteins, or DSRSI and  
 CC is useful for screening  
 CC a library of compounds  
 CC or development of a certain  
 CC innate immunity and/or  
 CC ligands are useful for  
 CC disorders, associated  
 CC (R). (R) is useful as  
 CC and the subunits DSRSI  
 CC antibodies or as anti-  
 CC encoding (R) are useful  
 CC variants from other in  
 CC represents the specific  
 CC composition of the pre  
 XX Sequence 150 AA;  
 SQ

Query	Match	11.4%	Score 4.00;	DB 20;	Length 150;
Best Local Matches	Similarity 78;	Pred. No. 9.	2e-24;	Indels 38;	Gaps 0;
Qy	14 LPKLALIPLILWYLFQTRPOGSAGPLOQCYGYGPLGDLNCSMWEPLGLDGAPESELHILQSQKY	73			
Db	23 Iptlellimsl1gprspqspqcyssgplglnscspeglietppvlyiqsqky	82			
Qy	74 RSNKQTQVAAAGRSHWVAIPREQLTNSDKLILWGTAKQPLWPPVYFNLTQMKPNAPRL	133			
Db	83 hpnrvwvekvpsqswtippqeftnadklliwtgkgrpwssvnletqmkpdpqj	142			
Qy	134 GPDVDFS	14.0			
Db	143 fsvadvts	14.9			

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RESULT 1.0
AAW12771 standard; protein; 862 AA
ID AAW12771
XX AAW12771;
XX AC
XX DT 12-MAY-1997 (first entry)
XX DE Human interleukin+12 beta-2 receptor
XX KW Interleukin-12 beta-2 receptor; IL-
KW rheumatoid arthritis; inflammatory
KW multiple sclerosis.
XX OS Homo sapiens .
XX FH key
FT Peptide 1..23
FT /label= Sig_peptid
FT Domain 24..62
FT /label= Extracellular
FT Domain 623..646
FT /label= Transmembrane
FT

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FT	Region	132..145	/label= Cytokine_receptor-motif		CC bowel disease and multiple sclerosis. The receptor protein or complex can also be used to detect (ant)agonists of IL-12 activity.
FT			/note= "cytokine receptor superfamily motif (Cys12..Cys413W)"		CC
FT	Region	305..309	/label= Cytokine_receptor-motif		CC
FT			/note= "cytokine receptor superfamily motif (W305RWS)"		CC
FT	Modified-site	47..50		Query Match 10.9%; Score 380; DB 18; Length 862;	XX
FT	Modified-site	129..131	/label= N-linked_glycosylation_site	Best Local Similarity 25.3%; Pred. No. 3.5e-21;	SQ
FT	Modified-site	166..168	/label= N-linked_glycosylation_site	Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;	Sequence 862 AA;
FT	Modified-site	186..188	/label= N-linked_glycosylation_site	Qy 31 RPQGSAGPLQCYGVGPLDILNCSWEPLGD-----LGAPSEIHLHQSO-----	31
FT	Modified-site	195..197	/label= N-linked_glycosylation_site	Db 126 qpqn---lsciqkqeqgtvactwergdrthlyteylqlsqgpknlwtqkcdiydy 181	126
FT	Modified-site	271..273	/label= N-linked_glycosylation_site	Qy 72 -----KYRSNKTQTV-AVAAGRSWVAAIPREQLTMSDKLLYWGTAKAGPQLNWPVFVN 121	72
FT	Modified-site	347..349	/label= N-linked_glycosylation_site	Db 182 dfqinltpespnfraktcavnslgssslp-stftfldv-----rpl-ppwdir 231	182
FT	Modified-site	76..378	/label= N-linked_glycosylation_site	Qy 122 LETOMKPNAPNLGPVDYFSEDDPLLEAVHNRAPPWPSHKVYLICQHYRRCOEAATLLEP 181	122
FT	Modified-site	480..482	/label= N-linked_glycosylation_site	Db 232 ikfq-havsr-----ctlywr---degivlnirxprpsnrlwnm--- 269	232
FT	Region	667..669	/label= Conserved_box_motif	Qy 182 ELKTIPLTPV---EIQDPLELATGKVYGRCRMKEEDLNGEWSPPLSFQTP---PSA朴 234	182
FT			/note= "conserved motif of cytokine receptor superfamily"	Db 270 ---vnvtakgrhdlldkpfteyefqskkhlykgswsdwseslratgppeetgtml 325	
FT	Region	699..704	/label= Conserved_box_motif	Qy 235 DVWVSGNLCGTCGGEBPLLMW-----AFGPCYDVSKYKWFVGRELSP--GTCCC 286	235
FT			/note= "conserved motif of cytokine receptor superfamily"	Db 326 dvwyymkrhidy-srqisqtlwknsveakqklihyqvtqeltgkamcnightswt 384	
FT	Region	786..798	/label= Conserved_box_motif	Qy 287 SLIPSGAEWA-RVSAVNA-TSWEPLNTNLVCLDSASAPRSVAVSSIAGSTELLYWQP 343	287
FT			/note= "conserved motif of cytokine receptor superfamily"	Db 385 tviprtgnwavaansksksslprrnniciegllapqvsans-esmdnvlvtwqp 443	
FT	Region	26-FEB-1997.	/label= Conserved_box_motif	Qy 344 --GPGEPLBHVWDWAR---DGDPGLEKLKNWVRLPPGPNLSALLPGNFTVGPYRITYAVS 397	344
FT			/note= "conserved motif of cytokine receptor superfamily"	Db 444 prkdpsavgeyyveerlhpqdtqvplnwrsrpynvsalseniksyicyervvays 503	
FT	Region	23-JUL-1996;	/label= Conserved_box_motif	Qy 398 ASGLASSSTWGFRRELAPLVGPTLWRLQDAPPGTPAIAENGEVPRHQLRGHLTHYC-- 455	398
FT			/note= "conserved motif of cytokine receptor superfamily"	Db 504 qd-99ccsilqngskhkaplsphinite-ekgsiliswnsipvgemqgcllyryiwk 561	
XX	EP759466-A2.			Qy 456 -AQSGTSPSYC---MNVSQNTQSVTLPDLPWGPCEBLWTAITGQGPCPILRLHLPDN 511	456
PN				Db 562 erdsnsqqplceipvrsgqshpinslq-prvtylwmcaltaqeshgnerefc1-q9 619	511
PD				Qy 512 TLRWK--VLPGI---LFVFLNLLGCGGLSLATSGRCYHLRKVLF-----PRNWKEVY 559	512
FT				Db 620 kanmvafapsiciainvgif-----sthyfqkvfvillaalrpqwcsrcip 667	559
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.			Qy 560 DPANSSSGQPH---MEQVPEAQPLGDLPILEVEEMPPVMMESSQQDATA---PLD 610	560
XX	Gubler UH,	96EP-0111807.		Db 668 dpanstarkyplaeektqlpldrliidppte---dpeplivsevlhqvtptvfrhppc 723	610
XX		30-MAY-1996;		Qy 611 SGYEKHFLPPIPPEEGLLG-----PPRPOVY 635	611
PR		96US-0018674.		Db 724 snwpq----rekgighqasekdmmhsassppppai 756	635
PR		01-AUG-1995;		RESULT 11	
DR		95US-0001701.		ID AAR11741 standard; Protein; 783 AA.	
XX				XX AAR11741;	
PS	Claim 3; Page 24-29; 53pp;	English.		AC	
XX				XX AAR11741 (first entry)	
CC	New human interleukin-12 (IL-12) receptor beta-2 receptor (AAW12771)			DE Granulocyte colony stimulating factor receptor.	
CC	has a low binding affinity for IL-12, but when complexed with an			XX G-CSF; receptor; clone D-7.	
CC	IL-12 beta-1 receptor (see also AAW12772), forms a complex with a			OS Homo sapiens.	
CC	high binding affinity for IL-12. Its amino acid sequence was			XX	
CC	deduced from a composite cDNA sequence (AAW59731) obtained from human				
CC	lymphoblasts. IL-12 receptor beta-2 can be expressed on the				
CC	surface of transformed host cells, opt., as a complex with co-expressed IL-12 receptor beta-1, and used in therapeutic				
CC	compsns., pref. with at least 1 cytokine antagonist, to treat				
CC	autoimmune dysfunctions such as rheumatoid arthritis, inflammatory				





DB	342	----wrq-----	rqlprtqvqlfwkpvpleedsgrrgy-vvswrpsg	379	DR WPI; 1997-076879/07.
QY	309	-----LNLNS-----	-SAPRSVAISSLAGST-----	335	DR N-PSDB; AAT47100.
DB	380	qegalplcntstfhlpsgevalrvnsactsrtpvvfesrpaltrlhama	439	XX PT Recombinant granulocyte colony stimulating factor receptor - for diagnostic, therapeutic and research uses	
QY	336	---ELIVTWQPGPGEPLEHVVWDGDPLEKLN--WVRLPPGNLUSA-LILPGNFTVGVP	388	XX PS Claim 1; Fig 3; 15pp; English.	
DB	440	rdphslwqwpbpqpgqyqgqppassnsnktwmeqngtrqflkenirpfqj	499	XX CC An alternative form (AAW10486) of human granulocyte colony stimulating factor receptor (G-CSFR) (see also AAW10485), results from alternative splicing and a change in the reading frame, leading to a different C-terminal amino acid sequence. It is the product of a cDNA clone (AAT47100) isolated from a human placental library. Recombinant G-CSFRs, esp. soluble forms comprising the extracellular domain, or modified forms having inactivated CC N-glycosylation sites, altered KEX2 protease cleavage sites or conservative amino acid substns., can be produced in host cells. G-CSFR polypeptides are useful in diagnostic assays of G-CSF, and for raising antibodies of use in diagnosis and therapy. G-CSFR CC can also be used in therapy to bind or scavenge G-CSF.	
QY	389	YRITTYTAVASGLASASSASVWGEKEEFLAPLYGPTLWRLDAPPGTAAIWGEVPRHQLRGH	448	XX SQ Sequence 800 AA;	
DB	500	yeiivpplqdtmgpdeqhvaysgemaphapel-hlkhighktwaglwrpeppelgksp	558	Query Match 8.5%; Score 297 5; DB 18; Length 800;	
QY	449	LHYTTLCAQSNSPSVCMNVSGNTQSVTLPDPWGCEWL-----VTA	491	Best Local Similarity 22.8%; Pred. No. 9e-15; Matches 158; Conservative 74; Mismatches 252; Indels 209; Gaps 33;	
DB	559	lhytlfwtwngqsfsailnassrgfvhle-paslyihlmaasqgatnstvtl	616	Db 140 lincwepqppethlpsftksfszgnccqggdslldcvpkdgsghccsprkhhllyqm 199	
QY	492	STIAGQSPPPGPPPLRLRUDNTLWKVFLPGFLFLWGLFL---GGCGLSLATSGRCYHLRK	548	Qy 50 LNCSEPLGLDGAPSELHLOSQKYSRSN-KTQTVAV----AAGRSMWVAPIREQLTMSDKL 103	
DB	617	miltpegs----elhi-----11qfglillitlcg----taulccspnkr	655	Db 140 lincwepqppethlpsftksfszgnccqggdslldcvpkdgsghccsprkhhllyqm 199	
QY	549	VLPRTWWEKVDPDANSSSG-----QPHMEQVP--EAQPIGLDPLILEVEEMEPPP-----	595	Qy 104 LVW----GTKAQOPLW-----PPVFVNLETQMKPNAPRLG-----PDVDF 139	
DB	656	--np1wpsvpdpahsllgswvptimedaaq1qlq1gtppkltkyleedekkpypwesh	712	Db 200 giwvqaenagtmsmssqlqk1dpmdvrvk1eppmlrtmdpsbaapqqac1qlqcwep---- 255	
QY	596	-----YMESSOPAQATAP-LDSGYERKHFLDTPEEJGLGPFR	631	Qy 140 SEDDPLEATVHWAPTPWSHKVLLICQF-HYRRCQEAAWTLLPELKTIPLTPVEIQDIEL 198	
DB	713	assetcg1ptivqtv1lgdpavstcqpsqsg-----tsdq--agppr	754	Db 256 -----wqqlghinhd---celrnkprqgeaswalgp-----lplealqya 294	
RESULT				Db 295 cgllpataytq1rcirwp1pghwdwspseirteraptrvltdt----- 341	
ID	AAW10486	standard; Protein; 800 AA.		Qy 251 PLLWKAPEGPCVQSYKXWWVWGGRELSPRGITCCCLSLIPSGAEMARSAVNTSWEP-- 308	
XX	AAW10486;			Db 342 ---wqr-----rqldprtqvlfwkpvpleedsgrrgy-vvswrpsg 379	
AC				Qy 309 -----LTNLS-----LVCLDSA-SAPRSVAISSLAGST----- 335	
DT	27-APR-1997	(first entry)		Db 380 qagailplclntstcfhlpseadevalraynsaqtstp:pvvfssergrpaltrhama 439	
XX	Human granulocyte colony stimulating factor receptor.			Qy 336 ----ELVLTWQPGPGEPLEHVVWDGDPLEKLN--WVRLPPGNLUSA-LILPGNFTVGVP 388	
KW	Granulocyte colony stimulating factor receptor; G-CSFR; diagnosis;			Db 440 rdphslwqwpbpqpgqyqgqppassnsnktwmeqngtrqflkenirpfqj 499	
KW	therapy.			Qy 389 YRITYAVASGLASASSVWGEKEEFLAPLYGPTLWRLDAPPGTAAIWGEVPRHQLRGH 448	
OS	Homo sapiens.			Db 500 yeiivtptydttmgpsqhvyyqgmapshape1-hlkhighktwaglwrpeppelgksp 558	
XX	Key Location/Qualifiers			Qy 449 LTHYTLCQAQSCTSPSVCMNVSGNTOSVTLDDLPNGPCELN-----VTA 491	
FT	Peptide	1..24		Db 559 lthytifwtiaqngfsa1nassqfvhle-paslyihlmaasqgatnstvtl 616	
FT	Protein	/label <sub>1..24</sub>		Qy 492 STIAGQSPPPGPPPLRLRUDNTLWKVFLPGFLFLWGLFL---GGCGLSLATSGRCYHLRK 548	
FT	Label <sub>1..24</sub>	25..783		Db 617 mt1pegs----elhi-----19f9111111c1cp-----lawlccspnkr 655	
FT	Domain	628..653		Qy 549 VLPRWWWEKVPDPANSSG-----QPHMEQVP--EAQPIGLDPLILEVEEMEPPPVMES 599	
FT	Misc-difference	/label <sub>1..24</sub> Transmembrane_domain		Db 656 --np1wpsvpdpahsllgswvptimedaaq1qlq1gtppkltkyleedekkpywes 711	
XX	/note= "alternative C-terminal sequence."			Qy 600 SQAQATAPLDGSYEKHFLLPTEELGLL-GPPR 631	
PN	US5589456-A.				
XX	31-DEC-1996.				
XX	26-SEP-1989;	890S-0412816.			
XX	24-SEP-1990;	900S-0587329.			
PR	26-SEP-1989;	890S-0412816.			
PR	03-OCT-1989;	890S-0416306.			
PR	03-APR-1990;	900S-0522952.			
PR	15-JAN-1993;	930S-0006183.			
PR	02-FEB-1995;	950S-0382771.			
XX	(IMMV ) IMMUNEX CORP.				
XX	Curtis LM, Larsen AD,	Sims JE,	Smith CA;		
P1					
X1					



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Qy 61 GAPSELHQSOKYRSNKTQTVAVAAGRSWVAIPREOLTMSDLVWGTAKQQPLNWPPVFV 120  
 Db 61 GAPSELHQSOKYRSNKTQTVAVAAGRSWVAIPREOLTMSDLVWGTAKQQPLNWPPVFV 120  
 Qy 121 NLETOMKPNAPRLGPDVDFSEDDPLEATVHWAAPTPNSHKVYLICOFHYRRCQEAAWTLL 180  
 Db 121 NLETOMKPNAPRLGPDVDFSEDDPLEATVHWAAPTPNSHKVYLICOFHYRRCQEAAWTLL 180  
 Qy 181 PELKTIPLTPVIEQDLETLATGYKVYGRCRMKEEDLWGENSPILSFRTOPPSAPKDQWVG 240  
 Db 181 PELKTIPLTPVIEQDLETLATGYKVYGRCRMKEEDLWGENSPILSFRTOPPSAPKDQWVG 240  
 Qy 241 NLCTGPGEPEPILLWAPGPVCQVSXKWWFVNGRELSPECITCCSLLSGAENARVSA 300  
 Db 241 NLCTGPGEPEPILLWAPGPVCQVSXKWWFVNGRELSPECITCCSLLSGAENARVSA 300  
 Qy 301 VNATSWEPLTNLSLVCDSDASAFRSVAVSSTAGSTELLVTWQPGPGEPLEHVWDWARDGD 360  
 D [REDACTED] 301 VNATSWEPLTNLSLVCDSDASAFRSVAVSSTAGSTELLVTWQPGPGEPLEHVWDWARDGD 360  
 Qy 361 PLEKLNNVRVLPGNLSALLPGNFTSYVPRITVTAVASGLASASSYWGPREELAPVGP 420  
 Db 361 PLEKLNNVRVLPGNLSALLPGNFTSYVPRITVTAVASGLASASSYWGPREELAPVGP 420  
 Qy 421 TLWRLQDAPPGTPAIAANGEVPHQQLRGLHTYTLCAQSGETSPSVCMNVSGNTQSVLPLD 480  
 Db 421 TLWRLQDAPPGTPAIAWGEVPRHQQLRGLHTYTLCAQSGETSPSVCMNVSGNTQSVLPLD 480  
 Qy 481 PWGPCELWLWVTAATIAGQGPQGJLRHLHPDNTLWRKVLPGTFLNGLFLIGCGLSLATSG 540  
 Db 481 PWGPCELWLWVTAATIAGQGPQGJLRHLHPDNTLWRKVLPGTFLNGLFLIGCGLSLATSG 540  
 Qy 541 RCYHLRKVLPKWVWWKVPDPNSSSCQPHMEQVPAQPGDPLILEVEEMEPYPMESS 600  
 Db 541 RCYHLRKVLPKWVWWKVPDPNSSSCQPHMEQVPAQPGDPLILEVEEMEPYPMESS 600  
 Qy 601 QPAQATAPLDSCSYEKHFPLPTPEELGLLGPQPRQVLA 636  
 Db 601 QPAQATAPLDSCSYEKHFPLPTPEELGLLGPQPRQVLA 636

RESULT 2  
 US-09-073-594-5

; Sequence 5, Application US/09073594

; GENERAL INFORMATION:

; APPLICANT: James W. Baumgartner

; APPLICANT: Donald C. Foster

; APPLICANT: Frank J. Grant

; APPLICANT: Cindy A. Sprecher

; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESS: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, Gary E

; REGISTRATION NUMBER: 31 648

; REFERENCE/DOCKET NUMBER: 95 - 31

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6673  
 ; FAX: 206-442-6678  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 636 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Protein  
 ; US-09-073-594-5

Query	Match	Score	DB 2:
	Best Local Similarity	100.0%	Length 636;
	Matches	636;	Mismatches 0;
	Conservative	100.0%	Indels 0;
			Gaps 0;
Qy 1	MRRGGAPFWMLPKLALLPLWLFQTRPQSGACPQCYGVGPLGDLNCWSBPLGDL	60	
Qy 1	MRRGGAPFWMLPKLALLPLWLFQTRPQSGACPQCYGVGPLGDLNCWSBPLGDL	60	
Db 61	GAPSELHQSOKYRSNKTQTVAVAAGRSWVAIPREOLTMSDLVWGTAKQQPLAPPV	120	
Db 61	GAPSELHQSOKYRSNKTQTVAVAAGRSWVAIPREOLTMSDLVWGTAKQQPLAPPV	120	
Qy 61	NLETQMKPNAPRLGPDVDFSEDDPLEATWQAPPWPSKHLVICOHYRRCQEAAWTLL	180	
Db 121	NLETQMKPNAPRLGPDVDFSEDDPLEATWQAPPWPSKHLVICOHYRRCQEAAWTLL	180	
Qy 121	PELKTIPLTPVIEQDLETLATGYKVYGRCRMKEEDLWGENSPILSFRTOPPSAPKDQWVG	240	
Db 181	PELKTIPLTPVIEQDLETLATGYKVYGRCRMKEEDLWGENSPILSFRTOPPSAPKDQWVG	240	
Qy 181	NLCGTPGEPEPILLWAPGPVCQVSXKWWFVNGRELSPECITCCSLLSGAENARVSA	300	
Db 361	NLCGTPGEPEPILLWAPGPVCQVSXKWWFVNGRELSPECITCCSLLSGAENARVSA	300	
Qy 361	PELEKLNNVRVLPGNLSALLPGNFTSYVPRITVTAVASGLASASSYWGPREELAPVGP	420	
Db 421	PELEKLNNVRVLPGNLSALLPGNFTSYVPRITVTAVASGLASASSYWGPREELAPVGP	420	
Qy 421	TLMRQLDAPPGTPAIAANGEVPHQQLRGLHTYTLCAQSGETSPSVCMNVSGNTQSVLPLD	480	
Db 421	TLMRQLDAPPGTPAIAWGEVPRHQQLRGLHTYTLCAQSGETSPSVCMNVSGNTQSVLPLD	480	
Qy 481	PWGPCELWLWVTAATIAGQGPQGJLRHLHPDNTLWRKVLPGTFLNGLFLIGCGLSLATSG	540	
Db 481	PWGPCELWLWVTAATIAGQGPQGJLRHLHPDNTLWRKVLPGTFLNGLFLIGCGLSLATSG	540	
Qy 541	RCYHLRKVLPKWVWWKVPDPNSSSCQPHMEQVPAQPGDPLILEVEEMEPYPMESS	600	
Db 541	RCYHLRKVLPKWVWWKVPDPNSSSCQPHMEQVPAQPGDPLILEVEEMEPYPMESS	600	
Qy 601	QPAQATAPLDSCSYEKHFPLPTPEELGLLGPQPRQVLA	636	
Db 601	QPAQATAPLDSCSYEKHFPLPTPEELGLLGPQPRQVLA	636	

RESULT 3  
 US-09-275-925-5

; Sequence 5, Application US/09275925

; Patent No. 6080406

; GENERAL INFORMATION:

; APPLICANT: James W. Baumgartner

; APPLICANT: Donald C. Foster

; APPLICANT: Frank J. Grant

; APPLICANT: Cindy A. Sprecher

; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESS: ZymoGenetics, Inc.

; STREET: 1201 Eastlake Avenue East

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, Gary E

; REGISTRATION NUMBER: 31 648

; REFERENCE/DOCKET NUMBER: 95 - 31

; CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc. Street: 1201 Eastlake Avenue East City: Seattle State: WA COUNTRY: USA ZIP: 98102 COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0,  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/275,925  
FILING DATE:  
CLASSIFICATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-275-925-5

Query Match 100.0%; Score 3498; DB 3; Length 636;  
Best Local Similarity 100.0%; Pred. No. 1.7e-280; Mismatches 0; Indels 0; Gaps 0;

Matches 636; Conservative 0; Gaps 0;

Qy 1 MRGGGAPFWLPLPKLALLPLMVLQYPLQGKPLGDLNCSWEPGLDL 60  
Db 1 MRGGGAPFWLPLPKLALLPLMVLQYPLQGKPLGDLNCSWEPGLDL 60

Qy 61 GAPSEHLQSOKYRSNKTOVAVAAGRSRVAIPEQLTMSDKLUVGTRAGQPIWPPVY 120  
Db 61 GAPSEHLQSOKYRSNKTOVAVAAGRSRVAIPEQLTMSDKLUVGTRAGQPIWPPVY 120

Qy 121 NLETOMKPNAPRLGPDPDVFSEDDPLEATVHWAAPTWPSHKVYLICOFHYRCQEAWTLL 180  
Db 121 NLETOMKPNAPRLGPDPDVFSEDDPLEATVHWAAPTWPSHKVYLICOFHYRCQEAWTLL 180

Qy 181 PELKTIPLTPVEIQDLEATGKYKYGRCRMKEEDLWGENSPILSFQTPPSAPKDYWWSG 240  
Db 181 PELKTIPLTPVEIQDLEATGKYKYGRCRMKEEDLWGENSPILSFQTTPSAPKDYWWSG 240

Qy 241 NLCGTPGGEFPPLWIKAPGCVQSYKVNFWVGRELSPSEGITCCCLSPSGAEWARVSA 300  
Db 241 NLCGTPGGEFPPLWIKAPGCVQSYKVNFWVGRELSPSEGITCCCLSPSGAEWARVSA 300

Qy 301 VNATSWEPLTNSLVCLDSASAPRSVAVSSIASTGELTYTWQPGPGEPLEHHVVDWARDGD 360  
Db 301 VNATSWEPLTNSLVCLDSASAPRSVAVSSIASTGELTYTWQPGPGEPLEHHVVDWARDGD 360

Qy 361 PLEKUNWVRLPGNLSALPQFNTVGPYRITIVAVASGSLASASSVGRELAPLVGP 420  
Db 361 PLEKUNWVRLPGNLSALPQFNTVGPYRITIVAVASGSLASASSVGRELAPLVGP 420

Qy 421 TLWRIQDAPGTPAIAWGEVRPHOLRGHTHVTCAQSCSTSPTCMVNSGNTQSVTLPDL 480  
Db 421 TLWRIQDAPGTPAIAWGEVRPHOLRGHTHVTCAQSCSTSPTCMVNSGNTQSVTLPDL 480

Qy 481 PWGPGELWNTAATGQPPGPILRLHDPTNLWKVLPGLFLIGCGSLSATSG 540  
Db 481 PWGPGELWNTAATGQPPGPILRLHDPTNLWKVLPGLFLIGCGSLSATSG 540

Qy 541 RCYHLRKVLPRWWEKVDPDANSSSGQPHMEQYPEAQPGLDITLEVEEMEPVVMESS 600  
Db 541 RCYHLRKVLPRWWEKVDPDANSSSGQPHMEQYPEAQPGLDITLEVEEMEPVVMESS 600

RESULT 4  
US-08-653-740-3  
; Sequence 3, Application US/08653740  
; Patent No. 5192850  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 578 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-653-740-3

Query Match 90.1%; Score 3150; DB 1; Length 578;  
Best Local Similarity 90.9%; Pred. No. 7.7e-222;  
Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

Qy 1 MRGGGAPFWLPLPKLALLPLMVLQYPLQGKPLGDLNCSWEPGLDL 60  
Db 1 MRGGGAPFWLPLPKLALLPLMVLQYPLQGKPLGDLNCSWEPGLDL 60

Qy 61 GAPSEHLQSOKYRSNKTOVAVAAGRSRVAIPEQLTMSDKLUVGTRAGQPIWPPVY 120  
Db 61 GAPSEHLQSOKYRSNKTOVAVAAGRSRVAIPEQLTMSDKLUVGTRAGQPIWPPVY 120

Qy 121 NLETQMKPNAPRLGPDPDVFSEDDPLEATVHWAAPTWPSHKVYLICOFHYRCQEAWTLL 180  
Db 121 NLETQMKPNAPRLGPDPDVFSEDDPLEATVHWAAPTWPSHKVYLICOFHYRCQEAWTLL 180

Qy 181 PELKTIPLTPVEIQDLEATGKYKYGRCRMKEEDLWGENSPILSFQTTPSAPKDYWWSG 240  
Db 181 PELKTIPLTPVEIQDLEATGKYKYGRCRMKEEDLWGENSPILSFQTTPSAPKDYWWSG 240

Qy 241 NLETQMKPNAPRLGPDPDVFSEDDPLEATVHWAAPTWPSHKVYLICOFHYRCQEAWTLL 180  
Db 121 NLETQMKPNAPRLGPDPDVFSEDDPLEATVHWAAPTWPSHKVYLICOFHYRCQEAWTLL 180

Qy 181 PELKTIPLTPVEIQDLEATGKYKYGRCRMKEEDLWGENSPILSFQTTPSAPKDYWWSG 240  
Db 181 PELKTIPLTPVEIQDLEATGKYKYGRCRMKEEDLWGENSPILSFQTTPSAPKDYWWSG 240

Qy 241 NLCGTPGEEFPPLWIKAPGCVQSYKVNFWVGRELSPSEGITCCCLSPSGAEWARVSA 300  
Db 241 NLCGTPGEEFPPLWIKAPGCVQSYKVNFWVGRELSPSEGITCCCLSPSGAEWARVSA 300

Query Match 90.1%; Score 3150; DB 2; Length 578;  
 Best Local Similarity 90.9%; Pred. No. 7.7e-252;  
 Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;

---

RESULT 5  
 US-09-073-594-3  
 Sequence 3, Application US/09073594  
 Patent No. 592535  
 GENERAL INFORMATION:  
 APPLICANT: James W. Baumgartner  
 APPLICANT: Donald C. Foster  
 APPLICANT: Frank J. Grant  
 APPLICANT: Cindy A. Sprecher  
 TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/073,594  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARKER, Gary E  
 REGISTRATION NUMBER: 31,648  
 REFERENCE/DOCKET NUMBER: 95-31  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 578 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-073-594-3

QY 301 VNATSWPLTNLSVCLDSASAPRSVAVSSTAGSTELLVTQPGPGRPLEHIVVDWARDGD 360  
 Db 301 VNATSWPLTNLSVCLDSASAPRSVAVSSTAGSTELLVTQPGPGRPLEHIVVDWARDGD 360  
 QY 361 PLEKLNWVRLPGNLSALLPGNFTVGVPRITVTAASGLASSASSYWGREFEELAPLVGP 420  
 Db 361 PLEKLNWVRLPGNLSALLPGNFTVGVPRITVTAASGLASSASSYWGREFEELAPLVGP 420  
 QY 421 TWRQLDAPPGTPAANGEVPHQRLCHLTHTLCAOSGTSTVLPGLTFLWGLFLLGCGLSLATSG 540  
 Db 421 TWRQLDAPPGTPAANGEVPHQRLCHLTHTLCAOSGTSTVLPGLTFLWGLFLLGCGLSLATSG 540  
 QY 481 PPGPCPELWVTAATIAGQPPGPTLRLHPDNTLWRKVLPGLTFLWGLFLLGCGLSLATSG 540  
 Db 481 PPGPCPELWVTAATIAGQPPGPTLRLHPDNTLWRKVLPGLTFLWGLFLLGCGLSLATSG 540  
 QY 541 RCYHLRKVLPRWWKVPDPANSSQQPHMEQVPAQPLGDLPILEVEEMPPYMESS 600  
 Db 541 RCYHLRKVLPRWWKVPDPANSS----- 566  
 QY 601 QPAQATAPLDSSYEKHFLPPTPDELGLGGPPRFQVLA 636  
 Db 567 ----- -GLGGPPRFQVLA 578

RESULT 5  
 US-09-073-594-3  
 Sequence 3, Application US/09073594  
 Patent No. 592535  
 GENERAL INFORMATION:  
 APPLICANT: James W. Baumgartner  
 APPLICANT: Donald C. Foster  
 APPLICANT: Frank J. Grant  
 APPLICANT: Cindy A. Sprecher  
 TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/073,594  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARKER, Gary E  
 REGISTRATION NUMBER: 31,648  
 REFERENCE/DOCKET NUMBER: 95-31  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 578 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-073-594-3

QY 1 MRGGRGAPFWLMLPLPKLALLPLLWVLFQRTFRQGSAGPLOCYGVGPLGDLNCSWEPLGDL 60  
 Db 1 MRGGRGAPFWLMLPLPKLALLPLLWVLFQRTFRQGSAGPLOCYGVGPLGDLNCSWEPLGDL 60  
 QY 61 GAPSELHLQSQKYSRNSKTQTYAVAAGRSWVAIPREQLTMSDKLVLVNGTKAGQPLWPPVFV 120  
 Db 61 GAPSELHLQSQKYSRNSKTQTYAVAAGRSWVAIPREQLTMSDKLVLVNGTKAGQPLWPPVFV 120  
 QY 121 NLETQMKPNAPRIGPDVDFSEDDPLEATVHNPAPTWSHKYLICOPHYRRCQEAAWTLE 180  
 Db 121 NLETQMKPNAPRIGPDVDFSEDDPLEATVHNPAPTWSHKYLICOPHYRRCQEAAWTLE 180  
 QY 181 PELKTIPLTPVBIODLBATGKYVGRMRMEEDLWGENSPILSOTPPSAPKDQWVSG 240  
 Db 181 PELKTIPLTPVBIODLBATGKYVGRMRMEEDLWGENSPILSOTPPSAPKDQWVSG 240  
 QY 241 NLCTGPGEPEELWVKAQGPCVQSYKWFNYGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 Db 241 NLCTGPGEPEELWVKAQGPCVQSYKWFNYGGRELSPEGITCCCSLIPSGAEWARVSA 300  
 QY 301 VNATSWPLTNLSLVLCDSASAPRSVAVSSTAGSTELLVTWQPGPGRPLEHVWDWARDGD 360  
 Db 301 VNATSWPLTNLSLVLCDSASAPRSVAVSSTAGSTELLVTWQPGPGRPLEHVWDWARDGD 360  
 QY 361 PLEKLNWVRLPGNLSALPGNFTVGVPRITVTAASGLASSASSYWGREFEELAPLVGP 420  
 Db 361 PLEKLNWVRLPGNLSALPGNFTVGVPRITVTAASGLASSASSYWGREFEELAPLVGP 420  
 QY 421 TLWRQLDAPPGTPAIAWGEVPRHQLRGLTHYLCAQSGTSPSPVCMNNSGNTQSVTLPDL 480  
 Db 421 TLWRQLDAPPGTPAIAWGEVPRHQLRGLTHYLCAQSGTSPSPVCMNNSGNTQSVTLPDL 480  
 QY 481 PWGPCPELWVTAATIAGQPPGPTLRLHPDNTLWRKVLPGLTFLWGLFLLGCGLSLATSG 540  
 Db 481 PWGPCPELWVTAATIAGQPPGPTLRLHPDNTLWRKVLPGLTFLWGLFLLGCGLSLATSG 540  
 QY 541 RCYHLRKVLPRWWKVPDPANSSQQPHMEQVPAQPLGDLPILEVEEMPPYMESS 600  
 Db 541 RCYHLRKVLPRWWKVPDPANSSQQPHMEQVPAQPLGDLPILEVEEMPPYMESS 600  
 RESULT 6  
 US-09-275-925-3  
 Sequence 3, Application US/09275925  
 Patent No. 608406  
 GENERAL INFORMATION:  
 APPLICANT: James W. Baumgartner  
 APPLICANT: Donald C. Foster  
 APPLICANT: Frank J. Grant  
 APPLICANT: Cindy A. Sprecher  
 TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/073,594  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PARKER, Gary E  
 REGISTRATION NUMBER: 31,648  
 REFERENCE/DOCKET NUMBER: 95-31  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 578 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-073-594-3

Query Match 90.1%; Score 3150; DB 2; Length 578;  
 Best Local Similarity 90.9%; Pred. No. 7.7e-252;  
 Matches 578; Conservative 0; Mismatches 0; Indels 58; Gaps 1;



Qy 550 LPRWWKEVKPDDANSSSGQPHMEQVPEAQPLQDPLILEVEEMEPVVPMESSQPAQATAPL 609  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 548 LPQWIWERPDDANSNSGQPYIKEVSUPLQQPKDGPITLEVEELQPVVES --PKASAPI 604  
 Qy 610 DSGYEKHFLLPTPEELGLL 627  
 Db 605 YSGYEKHFLLPTPEELGLL 622

---

RESULT 8  
 Sequence 7, Application US/09073594  
 ; Patent No. 5923735  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James W. Baumgartner  
 ; APPLICANT: Donald C. Foster  
 ; APPLICANT: Frank J. Grant  
 ; APPLICANT: Cindy A. Sprecher  
 ; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/073, 594  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Parker, Gary E  
 ; REGISTRATION NUMBER: 31, 648  
 ; REFERENCE/DOCKET NUMBER: 95-31  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6673  
 ; TELEFAX: 206-442-6678  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 623 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-073-594-7

Query Match 58.4%; Score 2044; DB 2; Length 623;  
 Best Local Similarity 62.8%; Pred. No. 1.7e-160;  
 Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 14 LPKLALPLMLWLFQRTRPQGAGPQCYGVLQNCWPLGDGLGASELHQSQY 73  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 9 LTPLELLSLMSLLGTRPHSPGQLQCYSVGLTNCWPLGDLETPPVLYHQSQY 68  
 Qy 74 RSNIKTOVAYAAGRSNWAIPREQLTMSDKLWLWGTAKAGPLMPYFVNLTQMKPNAPRL 133  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 69 HPNRWKEVKPSKSNTIPREQTMDKLIWGTGRPIWMSVSVNLEQMKPPTPQI 128  
 Qy 134 GPDVDFSEDDPLLEATYHWAPETPSHKVLICQHYRRCQAATWLEPELKTIPLTPVEI 193  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 129 FSQVDISSEATYHWAPEWVPPKQALKCQFRYKECAEWTRLEPQLKTDGLTPVEM 188  
 Qy 194 QDLBLATGKVKYGRORMEKEEDLWGEWSPLSFQTPPSAKPDWWSGNLCTGPGBEPLL 253  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 189 QNLPESTCYQVSRCQVENGYP-WGEWSSPLSFQTPFELDWDVNSGTVCETSGKRALL 247

Query Match 58.4%; Score 2044; DB 3; Length 623;

Qy 254 LNKAPGPCVQSYKVNFVGGRELSPEGITGCCSLIPSGAEMARAVSANNATSWEPLTNLS 313  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 248 VWKDPREPCVQTYTVMNGADTTTQEVPCKSPVPMAMWAVVSPGNSTSWVPPNLS 307  
 Qy 314 LVCLDSASAPRSVVAASSLAGSTPELLTWQPGGEPLEHVWDARDGDPLEKUNWRLPG 373  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 308 LVCLAPASEAPCDVGVSADGSPGIKYTKWQGTRKPLEYVVDNAQDGDSLDKLWNTRLPG 367  
 Qy 374 NLSALLPGNFTVGVPYRITVTAVSAGLASASSVNGFREELAPLVGPTLWRLQDAPGTP 433  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 368 NLSTLPGFGRGVPYRITVTAVSGLAAAPSVMGFRREEPLVPLGAFFVWRLPDDPPTP 427  
 Qy 434 ATAWGEVPRHQLRQLHLLTHYLCAQSGTSTSVCNMVSGNTQSVTLPDLPWGPCBLWYTASt 493  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 428 YVAGWEVPRHQLRQATHYFCOSRGLSTCRNVSQSTOPATLPNHSSESKLWVYST 487  
 Qy 494 TAGQGPPGPIRLHLPDNTLRLKVLPOILFLMGLFLUGLGSLATS ---GRCYHLRKV 549  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 488 VAGQGPPGPDLSLHLPDNRIRKALPNFLSNGLLMGCGSLASPRCLQRCLHRHKL 547  
 Qy 550 LPRWWKEVKPDEANSSGGQPHMEQVPEAQPLQDLPITLEEEMEPPVYNESSQPAQATAPL 609  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 548 LPQWIWERPDDANSNSGQPVIKEVSLPQPKDGPITLEEEVEYLQPVES --PKASAPI 604  
 Qy 610 DSGYEKHFLLPTPEELGLL 627  
 |:|:|:|:|:|:|:|:|:|:|:  
 Db 605 YSGYEKHFLLPTPEELGLL 622

RESULT 9  
 US-09-275-925-7  
 ; Sequence 7, Application US/09275925  
 ; Patent No. 6080406  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James W. Baumgartner  
 ; APPLICANT: Donald C. Foster  
 ; APPLICANT: Frank J. Grant  
 ; APPLICANT: Cindy A. Sprecher  
 ; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/275, 925  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Parker, Gary E  
 ; REGISTRATION NUMBER: 31, 648  
 ; REFERENCE/DOCKET NUMBER: 95-31  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6673  
 ; TELEFAX: 206-442-6678  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 623 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-073-594-7

Query Match 58.4%; Score 2044; DB 2; Length 623;  
 Best Local Similarity 62.8%; Pred. No. 1.7e-160;  
 Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 14 LPKLALPLMLWLFQRTRPQGAGPQCYGVLQNCWPLGDGLGASELHQSQY 73  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 9 LTPLELLSLMSLLGTRPHSPGQLQCYSVGLTNCWPLGDLETPPVLYHQSQY 68  
 Qy 74 RSNIKTOVAYAAGRSNWAIPREQLTMSDKLWLWGTAKAGPLMPYFVNLTQMKPNAPRL 133  
 |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 69 HPNRWKEVKPSKSNTIPREQTMDKLIWGTGRPIWMSVSVNLEQMKPPTPQI 128  
 Qy 134 GPDVDFSEDDPLLEATYHWAPETPSHKVLICQHYRRCQAATWLEPELKTIPLTPVEI 193  
 |:|:|:|:|:|:|:|:|:|:|:  
 Db 129 FSQVDISSEATYHWAPEWVPPKQALKCQFRYKECAEWTRLEPQLKTDGLTPVEM 188  
 Qy 194 QDLBLATGKVKYGRORMEKEEDLWGEWSPLSFQTPPSAKPDWWSGNLCTGPGBEPLL 253  
 |:|:|:|:|:|:|:  
 Db 189 QNLPESTCYQVSRCQVENGYP-WGEWSSPLSFQTPFELDWDVNSGTVCETSGKRALL 247

Best Local Similarity 62.8%; Pred. No. 1.7e-160; Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

ATTORNEY/AGENT INFORMATION:  
NAME: Silverman, Robert A.  
REGISTRATION NUMBER: 35,682  
REFERENCE DOCKET NUMBER: CD 9195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-2863  
TELEFAX: (201) 235-2363  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 862 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-118-2

Query Match Score 380; DB 2; Length 862;  
Best Local Similarity 50.3%; Pred. No. 6.2e-23;  
Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Query 31 RQGSAGSAPLQCYGVGPQDNCWSWPLGD-----LGASEDFHLQSQ-----71  
Db 126 QPQN----LSCIQKQGEGQTACTWGRDTHLYTEYLQSLGPKNLTWQKCDIYCDYL 181  
Qy 72 -----KYSRNKTQTV-AVAAGRSWVAIPREOLTMDSKLVLYNGCTKAGOPLWPPFVN 121  
Db 182 DFGINLTPESSPEINTAKTAVNLSGSSSLD-STTFLDIV-----RPL-PWDIR 231  
Qy 122 LETOMKPNAPRUGPDYDFSEDDPLEATVHWRAPPTWPSKVLCIQHYRRQEAFTILEP 181  
Db 232 IKFQ-KASVSR-----CTLYWR----DEGLVLLNRURYRPSNSRLNNM---269  
Qy 182 ELKTIPLTPV---ETQDLEATAGKVKYGRCRMEKEIDLWEMSPISLFTQP--PSAPK 234  
Db 270 ---VNTVAKGRHDLLDKPTELEYQISSKHLKYGSNSDWSESURAQTPPEEETGML 325  
Qy 235 DVWVSGNLCGTPGGEBPLLNK-----APGPCVQSYKWFVGNGRLHESPE-GITCCC 286  
Db 326 DVWYMKRHIDY-SRQQTSFLFKNLNSYSEARGKILHYQVTLQBLTGKAMONTIGHTSWT 384  
Qy 287 SLIPSGAEWA-RVSAYNA-TSWEPILTNLNSLVCLDSSAAPSRSVAVSSIASTELLVWQ 343  
Db 385 TVIPRTGNWAVASAANSKGSSLPTINIMLCEAGLAPHQVSANS-EGMDNINLVWQ 443  
Qy 344 ---GCPSEPLEHHVDWAR--DGDPLBKLNWVRLPQCNLSALLPGNTVGVPYRIVTAVS 397  
Db 444 PRKDPSAVQEVYVNERELHPGDTQVPLNNLRSRPYNSALISENTSKYCIEIRYALS 503  
Qy 398 ASGLASASSWGVFREELAPLIVGPTLWRLDAPPGTIAJGEVPRHQLRGHLTHYTLC--455  
Db 504 GD-QGGCSSTLGNSHKAPLSGPHNIAITE-EKGSLISNSIPIQDMGCLLHYRIYWK 561  
Qy 456 -AQSGSTSPTSYC---MNNSGNTOSVTLPDLPNGPCELMWVTASTIAGQGPPGPILRLHLPDN 511  
Db 562 ERDSNSQPLQCEIPYRSQNSHPINSLQ-PRTYVLMWMTAAAGESHGNREFL-QG 619  
Qy 512 TLRWK--VLPGI--LFLWGFLLGCGLSLATSGRCYHLRKVL-----PRTWKVP 559  
Db 620 KANWMAFAPSPICIAIMYGF-----STHYFQOKVFVLLAALRPQWCSREIP 667  
Qy 560 DPANSSGQPH-----MEQVBEAQPLGDPITLEVEEMPPVMESSQAQATA---PLD 610  
Db 668 DPANSTCAKKYPIAEEKTQLPDRLLIDWTP-----DPEBLVISEVLHQVTPVERHPPC 723  
Qy 611 SGYEKFHFLPTPEEGLLG-----PPRFQVL 635  
Db 724 SNWPO----REKGIIQHORSEKDMMSASSPPBR 756

RESULT 11  
US-08-915-495-2  
Sequence 2, Application US/08685118  
Patent No. 580530  
GENERAL INFORMATION:  
APPLICANT: Gubler, Ulrich A  
APPLICANT: Flesky, David H  
TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: NJ  
COUNTRY: USA  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,118  
FILING DATE:  
CLASSIFICATION: 435

GENERAL INFORMATION:  
 APPLICANT: Gubler, Ulrich A  
 APPLICANT: Presly, David H  
 TITLE OF INVENTION: RECEPATORS FOR HUMAN IL-12  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 07110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/915,495  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/685,118  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silverman, Robert A.  
 REGISTRATION NUMBER: 35,682  
 REFERENCE/DOCKET NUMBER: CD 9195  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 235-2863  
 TELEFAX: (201) 235-2363  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 862 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-915-495-2

Query Match Score 10.9%; Score 380; DB 2; Length 862;  
 Best Local Similarity 25.3%; Pred. No. 6.2e-23;  
 Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Qy 31 REQSGAGPLCQVGPGDLDLNQSWEPLGD-----LGAPSEHLHQSQ----- 71  
 Db 126 QFQN---LSCIQKGEOTVACTWGRSVAIPEQLTMSDKLYNGCTKGQPLWPVFN 181  
 Qy 72 -----KYSRNTPESSPNATAKTVANSLSGSSSLP-----STFTFLDV----- 181  
 Db 182 DEGINLTPESSPNATAKTVANSLSGSSSLP-----STFTFLDV----- RPL-PWDIR 231  
 Qy 122 LETQMKPNAPIRGPDYDFESEDDPLEATVHNWAPTPWSHKVLICPHYRRCOEATLLEP 181  
 Db 232 IKFQ-KASVSR-----CTLYNR-----DEGLVILNRLRYPNSRLRNM--- 269  
 Qy 182 EIKTIPLTPV---EQDLELAETGKVYGRQMEKEEDLGEWSPLSFQTP---PSAPK 234  
 Db 270 ---VNVTKAHRHDLLDKTFTEYEFOQISQKHLYKGSSDWSLESLRATQPEEPTGML 325  
 Qy 235 DWVSGNLCGTPGEBPLWK-----APCPVQSYKQWVGGRELSPS--GITCCC 286  
 Db 326 DWYMKRHIDY-SRQQTSLFMKNLVSSEARSKILHXYQVTOQELTGKAMNTHTHTSWT 384  
 Qy 287 SLIPSGAEGA-RVSAVNA---TSEWEPLTNLSVCLDSASAPRSVAYSSIASTELLVWQP 343  
 Db 385 TVPRGWNWAVSAANSKGKSLLPRINMINLCEAGLARQVSANS-EGMDNLTWVQ 443  
 Qy 344 -GPGEPLEHVWDWR--DGDPGLEKLNWVRLRPPGNLALPGNFTGVYPRIVTAYS 397  
 Db 444 PRKDPSAVQEVENRELHPGDTQVPLNWRSRYNNVSALISENKSYICEIRVYALS 503  
 Qy 398 ASGLASASSYWGFREELAPLVGTLWRLQQDAPGTPTAIANGEVPRHQLRGLHTHYTLC -- 455

RESULT 12  
 US-08-914-520-2  
 Sequence 2, Application US/08914520  
 ; Patent No. 5919903  
 GENERAL INFORMATION:  
 ; APPLICANT: Gubler, Ulrich A  
 ; APPLICANT: Presly, David H  
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07110  
 COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/914,520  
 ; FILING DATE:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/685,118  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Silverman, Robert A.  
 ; REGISTRATION NUMBER: 35,682  
 ; REFERENCE/DOCKET NUMBER: CD 9195  
 ; TELEPHONE: (201) 235-2863  
 ; TELEFAX: (201) 235-2363  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 862 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-914-520-2

Query Match Score 10.9%; Score 380; DB 2; Length 862;  
 Best Local Similarity 25.3%; Pred. No. 6.2e-23;  
 Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Qy 31 RPQSGAGPLCQVGPGDLDLNQSWEPLGD-----LGAPSEHLHQSQ----- 71  
 Db 126 QPQN---LSCIQKGEOTVACTWGRSVAIPEQLTMSDKLYNGCTKGQPLWPVFN 181  
 Qy 182 -----LGAPSEHLHQSQ-----STFTFLDV-----RPL-PWDIR 231  
 Db 232 IKFQ-KASVSR-----CTLYNR-----DEGLVILNRLRYPNSRLRNM--- 269  
 Qy 183 EIKTIPLTPV---EQDLELAETGKVYGRQMEKEEDLGEWSPLSFQTP---PSAPK 234  
 Db 270 ---VNVTKAHRHDLLDKTFTEYEFOQISQKHLYKGSSDWSLESLRATQPEEPTGML 325  
 Qy 235 DWVSGNLCGTPGEBPLWK-----APCPVQSYKQWVGGRELSPS--GITCCC 286  
 Db 326 DWYMKRHIDY-SRQQTSLFMKNLVSSEARSKILHXYQVTOQELTGKAMNTHTHTSWT 384  
 Qy 287 SLIPSGAEGA-RVSAVNA---TSEWEPLTNLSVCLDSASAPRSVAYSSIASTELLVWQP 343  
 Db 385 TVPRGWNWAVSAANSKGKSLLPRINMINLCEAGLARQVSANS-EGMDNLTWVQ 443  
 Qy 344 -GPGEPLEHVWDWR--DGDPGLEKLNWVRLRPPGNLALPGNFTGVYPRIVTAYS 397  
 Db 444 PRKDPSAVQEVENRELHPGDTQVPLNWRSRYNNVSALISENKSYICEIRVYALS 503  
 Qy 398 ASGLASASSYWGFREELAPLVGTLWRLQQDAPGTPTAIANGEVPRHQLRGLHTHYTLC -- 455

Query Match Score 10.9%; Score 380; DB 2; Length 862;  
 Best Local Similarity 25.3%; Pred. No. 6.2e-23;  
 Matches 177; Conservative 88; Mismatches 272; Indels 162; Gaps 36;

Qy 31 RPQSGAGPLCQVGPGDLDLNQSWEPLGD-----LGAPSEHLHQSQ----- 71  
 Db 126 QPQN---LSCIQKGEOTVACTWGRSVAIPEQLTMSDKLYNGCTKGQPLWPVFN 181  
 Qy 182 -----LGAPSEHLHQSQ-----STFTFLDV-----RPL-PWDIR 231  
 Db 232 IKFQ-KASVSR-----CTLYNR-----DEGLVILNRLRYPNSRLRNM--- 269  
 Qy 183 EIKTIPLTPV---EQDLELAETGKVYGRQMEKEEDLGEWSPLSFQTP---PSAPK 234  
 Db 270 ---VNVTKAHRHDLLDKTFTEYEFOQISQKHLYKGSSDWSLESLRATQPEEPTGML 325  
 Qy 235 DWVSGNLCGTPGEBPLWK-----APCPVQSYKQWVGGRELSPS--GITCCC 286  
 Db 326 DWYMKRHIDY-SRQQTSLFMKNLVSSEARSKILHXYQVTOQELTGKAMNTHTHTSWT 384  
 Qy 287 SLIPSGAEGA-RVSAVNA---TSEWEPLTNLSVCLDSASAPRSVAYSSIASTELLVWQP 343  
 Db 385 TVPRGWNWAVSAANSKGKSLLPRINMINLCEAGLARQVSANS-EGMDNLTWVQ 443  
 Qy 344 -GPGEPLEHVWDWR--DGDPGLEKLNWVRLRPPGNLALPGNFTGVYPRIVTAYS 397  
 Db 444 PRKDPSAVQEVENRELHPGDTQVPLNWRSRYNNVSALISENKSYICEIRVYALS 503  
 Qy 398 ASGLASASSYWGFREELAPLVGTLWRLQQDAPGTPTAIANGEVPRHQLRGLHTHYTLC -- 455

542248-13  
 i APPLICANT: SMITH, CRAIG A.; LARSEN, ALF D.; SIMS, JOHN E.;  
 i SON, CURTIS M.  
 i TITLE OF INVENTION: DNA SEQUENCES ENCODING GRANULOCYTE-COLONY  
 i STIMULATING FACTOR RECEPTORS  
 i NUMBER OF SEQUENCES: 6  
 i CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/08/6,183  
 i FILING DATE: 15-JAN-1993  
 i PRIOR APPLICATION DATA:  
 i APPLICATION NUMBER: 587,329  
 i FILING DATE: 24-SEP-1990  
 i APPLICATION NUMBER: 522,952  
 i FILING DATE: 03-APR-1990  
 i APPLICATION NUMBER: 416,306  
 i FILING DATE: 03-OCT-1989  
 i APPLICATION NUMBER: 412,816  
 i FILING DATE: 26-SEP-1989  
 i SEQ ID NO: 2;  
 i LENGTH: 783  
 542248-2  
 Query Match 8.5%; Score 298.5; DB 6; Length 783;  
 Best Local Similarity 22.5%; Pred. No. 2.9e-16;  
 Matches 160; Conservative 75; Mismatches 250; Index 227; Gaps 34;

---

50 LNCWEBPLGLGAPSEHLQSOKYRSN-KTQTAVV-----AAGRSHWAIPREQLTNSDKL 103  
 Db 140 LICQWEPGPETHLPTSETLKFKSRGCGOTOGDSILCPKGOSCCPRKHLLYQNM 199  
 Qy 104 LVW-----GTTKAGQFLW-----PPVFVNLETQMKPNAPRLG-----PDVDF 139  
 Db 200 GIWQQAENALGTSMSPCQLCDPMVDYKLEPPMLRTMPSPEAPPQAGCLQLCWEP---- 255  
 Qy 140 SEDDPLEATVHWAPPWPSHVKYLICOP-HYRCQEAAWTLEPELKTIPLTPVEIQDEL 198  
 Db 256 -----WQGLHINQK--CEHRHKPORGAEASWALVG-----LPLEALQYEL 294  
 Qy 199 -----ATGYKVYGRCRMKEEIDLWGENSPILSFOTPPSAPK--DWMVSGNUGCTPGEE 250  
 Db 295 CGLPPATAYTQIRCTRWPLPHWSDISPSUBLRTTRAPTYVRDLW----- 341  
 Qy 251 PLLWKAPGPGCVQVSXKWFVNGREISPEGITCCCSLIPSGAEMARVSAYNTSWEP-- 308  
 Db 342 -----WRQ-----RQDPRTVQLENKPVPLEEDSGRIOGY VVSNRPSG 379  
 Qy 309 -----LTNLS-----LYCLDLSA - SAPRSVAVSSIAGST----- 335  
 Qy 380 QAGAILELCNTTELSCTFHLPSEAQEVALVAYNSAGTSRIPVFSERGPALTRHAMA 439  
 Qy 336 -----ELIYTWQPGPGEPELEYHDWARDGDPLEKL - WRLPPGNLNA - LLPGNFIVGV 388  
 Db 440 RDPHSILWGWEWPNPWQGTYIEWLGUPSASNNTWRMEONGRATGFJLKENIRFPQL 499  
 Qy 389 YRITYTAVASGLASASWVGFREEALPLVGPTLWRLQDAPPGTPATAWGEVPRHQLRG 448  
 Db 500 YEIVTPLYQDTMGPSQHVAYSQENMAPSHAPEL-HLKHKGTWQAILEWWPEPPLGKSP 558  
 Qy 449 LTHYTLCAGSQTSPSYCNVSCNTQSVPNLDPDWGPQELW-----VTA 491  
 Db 559 LTHYTFTWNAQNQSFATLNASSRGFLVHGLE--PASLYHTHLMASAQAGATNSTVLT 616  
 Qy 492 STIAGQPPGPILRHLPDNTLRWKVLPGLFILFWGLFL--GCGLSLATSRCYHLRK 548  
 Db 617 MTLTPES---ELH1-----IGLFLGLLTLTCG--TAWLCCSFNRK 655  
 Qy 549 VLPRWVYKEVDPDANSGG-----QPHMEOVP - EAQPLGDLPLTLEVEEMEPPP-- 595  
 Db 656 ---NPMLPSVPDAHSLSGSWPTIMBDAFOLPGLUTPTKLVLEEDERKPVWESH 712  
 Qy 596 -----MESSQPAQATAP - LDSGYKEHFLPPEELGLGPPR 631  
 Db 713 NSSETCGLPTLVQTYVILQGDPRAVSTQPQSOSG-----TSDQ --AGPPR 754

RESULT 14  
 US-07-923-976-4  
 i Application US/07923976  
 i Patent No. 5574136  
 i GENERAL INFORMATION:  
 i APPLICANT: Nagata, Shigekazu  
 i APPLICANT: Fukunaga, Rikitaro  
 i TITLE OF INVENTION: DNA Encoding Granulocyte Receptor  
 i NUMBER OF SEQUENCES: 8  
 i CORRESPONDENCE ADDRESS:  
 i ADDRESSEE: Jones, Tullar & Cooper, P.C.  
 i STREET: P.O. Box 2266 Eads Station  
 i CITY: Arlington  
 i STATE: Virginia  
 i ZIP: 22202  
 i COMPUTER READABLE FORM:  
 i MEDIUM TYPE: Floppy disk  
 i COMPUTER: IBM PC compatible  
 i OPERATING SYSTEM: PC-DOS/MS-DOS  
 i SOFTWARE: Patent Release #1.0, Version #1.25  
 i CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/07/923,976  
 i FILING DATE: 07-JUN-1993  
 i NUMBER OF SEQUENCES: 8

CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 74539/1990  
 FILING DATE: 23-MAR-1990  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 176629/1990  
 FILING DATE: 03-JUL-1990  
 PRIORITY APPLICATION DATA: PCT/JP91/00375  
 FILING DATE: 22-MAR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hellwege, James W.  
 REGISTRATION NUMBER: 28 808  
 REFERENCE/DOCKET NUMBER: 514853  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-415-1500  
 TELEFAX: 703-415-1508  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 836 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-923-976-4

Query Match Score 8.5% Best Local Similarity 22.8% Pred. No. 3 8e-16; Length 836; Matches 158; Conservation: 74%; Mismatches 252%; Indels 209; Gaps 33;

Qy 50 LNCWSWEPFLGDIQAPSELHQLQSOKYRSN-KTQTVAV----AAGRSWVAIPREQLTMSDKL 103  
 Db 140 LQCQWEGPPTIHPUTSTPLKSKRSRGNQCQDSDILCVPKDQSHCCIPKRHLIQQNM 199

Qy 104 LWV-----GTKAGQPLW-----PPVFVNLETQMKPNAPRLG-----PDVDF 139  
 Db 200 G1WQQAENALGTSMSPQCLDPMVYKLEPPMLRTMDPSPEAPPQAGCQLQWCWEP--- 255

Qy 140 SEDDPLEATVHKAPWTPWPKVHLICQE-HYRCQEAWTLLPELTKTIPVETQDDEL 198  
 Db 256 -----WQGLPHINQK--CELRHKPQGRGEANSWALPV-----LPLEALQYEL 294

Qy 199 -----ATGYKYMGRCRMEKEEDLWGPNSWPSLQFOTPSAK-----DVWWSGNICGTPGSEE 250  
 Db 295 CGLLPATAYTLQIRCIRWPLQHWSDMSPSLELRTERAPVRLDTW----- 341

Qy 251 PULLWKAPGPCVQSYKWKWVYGGRELSPGTCCCSLIPSQGAENWARSAVNATSNEP-- 308  
 Db 342 -----WRQ-----ROLDPRVYQLEFWKPVPLEDSGRIQGY-VVSWRPG 379

Qy 309 -----LTNL-----LYCLDSA - SAPSVAVSIAGST----- 335  
 Db 380 QAGAILPLCNTELSCTFHLPSEAVALVANSACTSRPTPVVESESRGPATRLHAMA 439

Qy 336 -----ELLVTWQGPGBPLEHVDWARDGDPLEKLN--WVRGPNGNFTVGVP 388  
 Db 440 RDPHSILWGVWEPBNPNWPQGYTIEWLGPPSANSNSKWTWRMEQNGRATGFLLKENIRPFQI 499

Qy 389 YRITVTAASGLASASSVNGFREELAPLYGPTLWRLQDAPPGTPAIAGEVYPRHOLRGH 448  
 Db 500 YE1IVPPLYQDMGPSPQHVAYSQENAPASHAEL-HLKHKTQWALEMWPEPELGKSP 558

Qy 449 LTHYTLCQAQSGTSPSVCMNVGNTQSVTLPDLPWGCELW-----VTA 491  
 Db 559 LTHYTLCWTFNQNQNSFSATLNASSRGPFLRLE-PASLYTHILMAASQAGATNSTVTL 616

Qy 492 STIAGOCPPGPILRLHLPDNTLRLWVLPGLWFLL---GGCISLATSGRCYHLRK 548  
 Db 617 MTLLTPEGS-----ELHI-----TIGLFGLLLTLCLCG---TAWLCCSPNRK 655

Qy 549 VLPRTWYKEVKDPANSSGG-----QPHMEQVP--EAQPLGDPLILEYEMEPPVMES 599  
 Db 656 --NPLMPSVPPDAHSSLGSSWVPTIMEADEAQPLGLGTPPTKLVLEDEKRPV-WES 711

Qy 600 SQPAQATAPLDSGYEKHFLPTPEELGLL-GPDR 631  
 Db 712 HNSSETGG-----LPTLVQTvvLQGDFR 734

RESULT 15  
 US-08-19-652-6  
 Patent No. 5831007  
 Sequence 6, Application US/08419652  
 GENERAL INFORMATION:  
 APPLICANT: Chua, Anne O  
 APPLICANT: Gubler, Ulrich A  
 TITLE OF INVENTION: INTERLEUKIN-12 RECEPTOR  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: New Jersey  
 COUNTRY: United States of America  
 ZIP: 07110-1199  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: PC compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/419,652  
 FILING DATE: 11-APR-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/248,532  
 FILING DATE: 31-MAY-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/094,713  
 FILING DATE: 19+JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kassi, Alan P  
 REGISTRATION NUMBER: 32142  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 235-4205  
 TELEFAX: (201) 235-3500  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 602 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 1..602  
 OTHER INFORMATION: /note/ "Represents residues 98 to 731 of human granulocyte colony-stimulating factor-receptor."  
 OTHER INFORMATION: factor-receptor."  
 US-08-419-652-6

Query Match Score 8.4% Best Local Similarity 22.7% Length 602;  
 Matches 149; Conservative 70; Mismatches 240; Indels 197; Gaps 30;

Qy 50 LNCWSWEPFLGDIQAPSELHQLQSOKYREN-KTQTVAV----AAGRSWVAIPREQLTMSDKL 103  
 Db 21 LICQWEGPGETHPLTSFTLKSEFSRGNCTQGDSILDCKVDPQSHCCIPKHHLIQQNM 80

Qy 104 LWV-----GTKAGQPLW-----PPVFVNLETQMKPNAPRLG-----PDVDF 139  
 Db 81 GIWQQAENALGTSMSPQCLDPMVYKLEPPMLRTMDPSPEAPPQAGCQLQWCWEP--- 136

Qy 140 SEDDPLEATVHKAPWTPWPKVHLICQE-HYRCQEAWTLLPELTKTIPVETQDDEL 198

Db 137 -----WOPGLHINQK---CELHKPQRGEASWALVGP-----LPLEAQYEL 175  
 Qy 199 -----ATGYKVYGRCRMKEKEFDLMEWSPISTFQDPPSAPK---DVWSSNNLCGTPGGEE 250  
 Db 176 CGLLPATAYTQIRCIRWPLPGLHWSDWSPSLELRPTERAPTVRDTW----- 222  
 Qy 251 FLLWKAPEGCQVSYKWWFGGRELSPEGITCCCGSLGAENARYSAVANATSWEPE-- 308  
 Db 223 -----WEQ-----RQDPTVQLEFWKPVPLEEDGRIQY-VVSWRPGG 260  
 Qy 309 -----LTNLS-----LVCLDSA--SAPRSVAVSSIAST----- 335  
 Db 261 QAGAILPLCNNTTELSCTFHLPSSEAQEVALAYNSAGTSRPTVYSESRSPALTRLHAMA 320  
 Qy 336 -----ELLVWQGPBPEPLEHVWDWARDGDPLEKLN--WWRLLPGNMSA-LLPGNFTVGVP 388  
 Db 321 RDPHSLWVGNEPPNPWPOGTYIENGPPSAANSKTKTWMEQNRTGFELLENTRPFQL 380  
 Qy 389 YRITYTAVSAGLGLASSSYNGFREELAPLYGPTLWRLQADPGTPAIANGEVPRHQLRGH 448  
 Qy 381 YEIVVPLIQTDMGSQHVIYASQEMAPSHAPEL-HLKHKIGTKTWAOLEWPEPPBLGKSP 439  
 Qy 449 LTHYLCAQSGETSPSVCMNYGNTQSVTLPDLPGPCELW-----VTA 491  
 Db 440 LTHYTIEWTNAQNGFSATLNASSRGFVHLGE--PASLYHILMAASQAGATNSTVLT 497  
 Qy 492 STIAQGQQPPDPLRHLHPDNTLWKVLPGLFLMGLFL--GCGLSLATSGRCYHLRK 548  
 Db 498 MTLTPEGS-----ELHI-----TGFLFCFLLLLTCLG-----TAWLCCSPNRK 536  
 Qy 549 VLPFRWVEKYDPANSSSG-----QPHMEQVP-EAQOPLGDLFILEVEEMEPPP 595  
 Db 537 --NPLWPSYDPAHSSLGSWVPTIMEEDAFQPOLGTGPPITKLTVLEDEKKVPP 589

Search completed: May 9, 2002, 06:04:24  
 Job time: 36 sec

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Protein - protein search; using sw model						
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E-value:	34.24					
Bit score:	1 MNRLVARLTPLELLSLSMS.....IYSGYKHFPLPTPEEIGLLV 623					
Sequence:	1539.804 Million cell updates					
Scoring table:	BLOSUM62					
Gapopen:	10.0 , Gapext 0.5					
Number of hits satisfying chosen parameters:	219241					
Minimum DB seq length: 0						
Maximum DB seq length: 2000000000						
Post-processing:	Minimum Match 0%					
Maximum Match 100%						
Listing first 45 summaries						
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1: pir1;*						
2: pir2;*						
3: pir3;*						
4: pir4;*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	2044	59.7	636	2	JN0047	class I cytokine
2	277	8.1	1097	2	SL7308	Leukemia inhibitory
3	270	7.9	918	2	A93337	membrane glycoprotein
4	261	7.6	783	2	JH0329	granulocyte colony
5	255.5	7.5	837	2	A34898	granulocyte colony
6	253	7.4	863	2	C88252	granulocyte colony
7	252	7.4	1092	2	JX0312	differentiation
8	244	7.1	917	2	I94699	glycoprotein 130
9	228	6.7	771	2	B82525	granulocyte colony
10	223	6.5	918	2	A44257	interleukin-6 subunit
11	165.5	4.8	581	2	I45771	prolactin receptor
12	163	4.8	622	2	A40144	prolactin receptor
13	163	4.8	1559	2	A4425	Bravo/N-CAM cell
14	161	4.7	878	1	A40091	interleukin-3 receptor
15	161	4.7	26926	1	I30334	titin, cardiac muscle
16	160.5	4.7	1895	2	M28828	hypothetical protein
17	158	4.6	1268	1	A39440	neural cell adhesion
18	154	4.5	895	2	S74225	leptin receptor
19	153	4.5	892	2	S68439	leptin receptor
20	153	4.5	894	2	S68437	leptin receptor
21	153	4.5	900	2	S68440	leptin receptor
22	153	4.5	1162	2	S68438	neural cell adhesion
23	153	4.5	1137	2	T30581	collagen alpha 1
24	151.5	4.4	2944	2	A5849	rig-1 protein -
25	151	4.4	1344	2	T43116	leptin receptor
26	148	4.3	1162	2	PC4184	fibronectin precursor
27	148	4.3	2477	2	S14428	hypothetical protein
28	146	4.3	13055	1	T15680	protein-tyrosine
29	145	4.2	2029	1	TDFFLK	protein-tyrosine

protein-tyrosine-p				
prolactin receptor				
prolactin receptor				
lactogen receptor				
lactogen receptor				
prolactin receptor				
plasmacytoma assoc				
fibronectin - Afri				
leptin receptor, S				
tenascin Y precurs				
prolactin receptor				
protein-tyrosine-p				
Down syndrome cell				
prolactin receptor				
prolactin receptor				
prolactin receptor				
MPL-P protein prec				

ALIGNMENTS

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RESULT 1
JW0047
    class I cytokinase receptor precursor - human
    N[Alternative names: WSX-1]
    C[Species: Homo sapiens (man)]
    C[Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000]
    C[Accession: JW0047]
    C[Accession: JW0047]
    R[Sprecher, C.A.; Grant, F.J.J.; Baumgartner, J.W.; Presnell, S.R.; Schrader, S.K.]
    B[Biochem. Biophys. Res. Commun. 246, 82-90, 1998]
    A[Title: Cloning and characterization of a novel class I cytokine receptor.]
    A[Reference number: JW0047; MUID:98265921]
    A[Accession: JW0047]
    A[Molecule type: mRNAs]
    A[Residues: 1-636 <SPRO>]
    A[Cross references: GB:AF053004; NID:93153240; PID: AAC39755.1; PID:93153241]
    A[Experimental source: brain]
    C[Genetics];
    A[Map position: 19p13.11]
    C[Keywords: glycoprotein]
    F[1-32/Domain: signal sequence #status predicted <SIG>]
    F[515-540/Domain: transmembrane #status predicted <TM>]
    F[554-561/Domain: cytoplasmic #status predicted <CTP>]
    F[51, 76, 302, 311, 374, 382, 467/Binding site: carbohydrate (Asn) (covalent) #status

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Qy	368	NLSTLPGFEGKGVPRYITVAVSGLAAAPSAFPWVRLPDDPGTP 427
Db	374	NLSALLEPGNFTVGVPRITVAVSGLAAASSTWGFRRELAPLVGPTLRLQDAPGT 433
Qy	428	VVAGGEVPRQLRGQATHYTFCIQSGLISVCRNVSQTATLPLNHSSEFKLTVST 487
Db	434	ATAWGEVPRHOLRGHLTHYTLCQAQSTSPTSPYCMNSGNTQSUTLPNPGCELMVATST 493
Qy	488	VAGQGPPGPIDESLAHDNRKWLDPFLSLWGLLIMGGUSLASTRCIARCLHWRKHL 547
Db	494	IAGQQGPGPITRHLRDLNTWRKVLPGTLLWGLLIMGGUSLASTRCIARCLHWRKHL 549
Qy	548	LPOWITNERVPDANSNSGQPIKEYSLPQPDKGPILEVEELQPVYES--PKASAPI 604
Db	550	LPRWWEKVPDANSNSGQPMIEQVPEAQPLGDPLILEBEMPPVMMESSQPAQATPL 609
Qy	605	YSGYERKHFLTPPEELGLL 622
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S17308	Leukemia inhibitory factor receptor - human	
C;Species:	Homo sapiens (man)	
C;Date:	22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999	
C;Accession:	S17308	
R;Gearing, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Price	EMBO J. 10, 2839-2846, 1991	
A;Title:	Leukemia inhibitory factor receptor is structurally related to the IL-6 signal	
A;Reference number:	S17308; MUID:92007727	
A;Status:	preliminary	
A;Molecule type:	mRNA	
A;Residues:	1-109 <SEA>	
A;Cross-references:	GB:X61615; NID:934365; PIDN:CAA43805.1; PID:934366	
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Best Local Similarity	21.7%	Pred. No. 3e-11; Gaps 37;
Matches	143; Conservative	Mismatches 110; Mismatches 263; Indels 144; Gaps 37;
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Qy	80	SKQSW---VTPADKLINQTKQGPQSVLQMKDTPQF 129
Db	389	TNESTQQLFQMLPNQEYNTL-----NAHNPLGRSQSTILVNITEKVYHHTPTSF 439
Qy	130	SQDISEEATLEATYQWAPPWPEQPKQAKALTCQFYKECQAEAWTRLEPOLKTGTLTP---- 185
Db	440	KVKDINSTA---VKLSWHLGIFNFAKINFLEIEIKSNS---YOEQRNTVTKGENSSYL 493
Qy	186	YEMQNLEPGTCYQVSGRGCQENGYPWGENSSPLSFQTPFELDPE---DVWWSGTVCETSGK 242
Db	494	VALDKLNPTVLTFRICSTETWKWSKRNKQKHLTEASPSKGPDTRNEWS---SDGK 550
Qy	243	RAALWYKDPFPCVQ---VTTYTFWEGACDITQEEYVCCKEPVANE----WAVY 292
Db	551	N-LIITWK-P LPDNEANGKIIISIYNSCSSLDETOQSLSEIPDPQHKAEIRIDKNDXIIISV 608
Qy	293	SPGNSTSWVPPTNLSUVCLAPESPACDVGSSADG-SPGKIVTKWQGTRKPLEYVDWQ 351
Qy	609	AK-NSVGSPPSPSKIA---SME1PNDLKLKEQVYGMGKGLLTHYDPNNTCDVTKWCN 663
Db	352	DGDSLSDLK-NWTRLPGNLNLTLPLPS-EFRGKGPYRITVAVYSGGLAAAPSWMGREFEELV 409
Qy	664	SSRSEPCLMQWRKVPSNSLTSVIESDEFRIGIRNFYLFCRNQGYQQLRSMIGYEELA 723
Qy	348	DWAQDGDSLSDKLNLTRLPGNLNLTLPLPSLPGFEGKGPYRITVAVYSGGLAAAPSWMGREFEELV 456
Qy	410	PLAGPAVWRLLPDPGTPVWVAVGEYPRHOLRGQATHYT-CIOSRGLS 407
Qy	457	TVCRNVSSQTO-TATLPLNL-SGSFLKWLWTVSTVAGQGPDPDLSLHL - PDNR1RKWKL 512
Db	783	IKVRNNTDISQTKLRLADQGKTSFHVLRAYT---DGGVGPERSMMVVTKENSY---- 834
Qy	513	PWFSLWGLL---LMGCCGLSLASTRCIQLARCLHWRKHLPOWTR---VP 557
Db	835	-----GLTIAILIPVAVIVGY---VTSILCYRKR-----EMIKEFTYDPIP 874
Qy	558	DPANSNS-----GQPYTKEYSL-PQPDKDGPLIE-----VEEVE-LQPVESPK 599
Db	875	NPENCRAHQFQK\$YCEGSSALKTLEMNPCTPNVYEVLETSAFPKIEDTEBISVVARPE 934
RESULT	3	
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C;Species:	Homo sapiens (man)	
C;Date:	12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000	
C;Accession:	A36337	
R;Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.	Cell 63, 1149-1157, 1990	
A;Title:	Molecular cloning and expression of an IL-6 signal transducer, gp130	
A;Reference number:	A36337; MUID:91084844	
A;Accession:	A36337	
A;Molecule type:	mRNA	
A;Cross-references:	GB:M57230; PIDN:AAA5915.1; PID:9186354	
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A;Map position:	5q11-5q11	
C;Superfamily:	cytokine receptor homology	
C;Keywords:	glycoprotein; membrane protein	
F;134-316/Domain:	cytokine receptor homology <CRS>	
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Db	118	ITIISGLPPE-KPKNLSCLV-UNEGKMRCEWD---GCRET-----H-----LETNF 158
Qy	79	PSKQFWVTIPREQTMADKILINGTKQGPRLPWSSS-----VNLET----- 119
Db	159	TLKSWAT-----HFKPADCXAKRDPPTSCIVDSTVYFVNIEWWVAENALGKVTS 209
Qy	120	-----QMKPDTPQIFSQVDISSEATLEATYQWAPPWVPPQKAATCQFYKECQAEA 170
Db	210	DHINPDFVVKVKNPHNLSVIN-SEELSSILKLTWTNSKSIYSTILKNIQYTKDAST 268
Qy	171	WTRLEPLQLTDQIIPVEMONLQEPGTQYQVSGRGCQEVNGP-WGEMS---SPLSRQTPFLD 226
Db	269	WSQ1PPEDTASTRSSSETVQDLKPFTYVFRICMKDGYWSDWESEASGTYVEDRPSK 328
Qy	227	PEDWVWSGTVCTEGSKRAALQHPTWVQWVWQHDPFRCR-----VQVTTW----- 263
Db	329	APSEWYKIDPSHTQGYRTVQVWKTLPPEBANGKILDYEVTLTRPKSHLQNQYVNTAKLT 388
Qy	264	-----FAGADITTTQEVPPCC---KSPV-----PAMMEWAVV 292
Db	389	VNLNTNDRYLATLTVRNLYCKSDAAYL---TIPACDFQATIPVMDLKAIFPDNM1RWVW---T 444
Qy	293	SPGNST-----SMWPPTNLSVCLAPESPACDVGVSADGSPGKIVTKWQGTRKPLEYVV 347
Db	445	TPRESVKYLEW-----CVLSDKAP-----IT 466

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5
Searched:	100059 seqs,	36664827 residues
Number of hits satisfying chosen parameters:	100059	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0%	
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	Listing first 45 summaries	
Database :	SwissProt_39;*	
Pred.	No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
<b>SUMMARIES</b>		
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2	339.5	9.9 874 1 I12S_MOUSE
3	277	8.1 1097 1 I12R_HUMAN
4	270	7.9 918 1 I16B_HUMAN
5	261	7.6 836 1 GCSR_HUMAN
6	25.5	7.5 837 1 GCSR_MOUSE
7	252	7.4 1092 1 L1ER_MOUSE
8	244	7.1 917 1 IL6B_MOUSE
9	223	6.5 918 1 IL6B_RAT
10	177	5.2 581 1 PRUR_CEBEL
11	165.5	4.8 581 1 PRUR_BOVIN
12	163	4.8 622 1 PRUR_HUMAN
13	158	4.6 1284 1 NRCA_CHICK
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15	154	4.5 639 1 CAIC_RAISE
16	153	4.5 1162 1 LEPR_MOUSE
17	151.5	4.4 2944 1 CAL7_HUMAN
18	148	4.3 1162 1 LEPR_RAT
19	148	4.3 2477 1 FINC_RAT
20	145	4.2 2029 1 LAR_DROME
21	142.5	4.2 610 1 PRUR_RAT
22	142.5	4.2 1711 1 PTPO_RAT
23	142	4.1 1705 1 PTPO_MOUSE
24	14.2	4.1 3067 1 CAIC_MOUSE
25	140.5	4.1 616 1 PRUR_RABIT
26	140.5	4.1 2012 1 DSCA_HUMAN
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30	138.5	4.0 896 1 CYRB_MOUSE
31	138	4.0 897 1 CYRB_HUMAN
32	138	4.0 1493 1 NEOL_MOUSE
33	137	4.0 2481 1 FINC_XENELA

ALIGNMENTS					
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DT	20-AUG-2001 (Rel. 40, Created)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR (IL-12 RECEPTOR BETA-2)				
DE	(IL-12R-BETA2).				
GN					
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TAXID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	Pubmed-8943050;				
RA	Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y., Gately M.K., Gubler U;				
RT	"A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits."				
RL	Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).				
CC	-1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY				
CC	-1- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.				
CC	-1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
CC	-1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
DR	EMBL: U64198; AAC36675.1; -.				
DR	PRoteIN: SM00060; FN3; 3.				
DR	PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.				
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.				
FT	SIGNAL 1 21				
FT	CHAIN 22 862				
FT	DOMAIN 22 624				
FT	TRANSMEM 625 641				
FT	DOMAIN 642 862				
FT	DOMAIN 224 306				
FT	DOMAIN 421 508				

FIBRONECTIN TYPE-III 3.									
Query	Match	Score	Length	DB	FT	FT	FT	FT	FT
DOMAIN	519	607	3						
CARBHYD	48	48	3	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)
CARBHYD	129	129	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
CARBHYD	166	166	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
CARBHYD	195	195	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
CARBHYD	271	271	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
CARBHYD	347	347	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
CARBHYD	376	376	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
CARBHYD	480	480	3	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SEQUENCE	862 AA:	97134 MW:	6720E0D946B8DD58 CRC64;						
33;									
Query Match	11.2%	Score 384;	DB 1;	Length 862;					
Best Local Similarity	25.1%	Pred. No. 8.1e-20							
Matches	171;	Conservative	68;	Mismatches	281;	Indels	140;	Gaps	33;
Qy	5	RVARLTPLLELLSLSMILLGTRPHGSPGPQCYSVGPLGLNCSWEPILGD--LETPPVLY 62							
Db	102	KLACINSDEIQICAEIIFGVAFPE QPNQNSCIOKGEQTVACTIWERGRTHLTYEYLQ 160							
Qy	63	HQSQKYHPNRVWEYK-----VPSKQSQSWVTIPREQFTMDKLILINGTQKGR 107							
Db	161	LSGPK---NLTWQCKD1CYDYLDFGINUTPES-----N 204							
Qy	108	PLRSQSVNLLETQMKPDTOIQIFSQVDISSEATLAVTQWQAPPVWPP---QKA----- 156							
Db	205	SLGSSSS-----PSTFYFLDI-----VRPLP-WDIRIKEQAKASVSRCTI 244							
Qy	157	-----LTCQFRYKECQAEEAATRLEPOLKTDGLTPVMQNLEPGTCY-QVSQRCQE 206							
Db	245	YWRDEGLVLLNRLRVLRPNSRLWMNNVN--VTKAKGRHDIDLKPFTEBFQISSKLH 301							
Qy	207	NGPWGEWSSPLSFQTPFLDPE---DWVSGTVCETSGKRAALYWK----DPRPCV-- 256							
Db	302	KG-SWDWSESLRAQTPEEEPTGMLDVWYMKRHIDSROQISLF-WKNLSSVEARGSKLH 359							
Qy	257	-QVYTYYWFGAGDITTTQEVPCCKSPVPAMMEAW-VSEGNSTSWVPPPTNLSL--VCLA 312							
Db	360	YQTLQELTGKAMTONIGHTSNTVITPTGNWAVAVSANNSKGSSLPRINIMLCEA 419							
Qy	313	PESAPCDVGSSADCGPKTGTWKQTRKP---LEYVYDAQ--DGDSIDKLWTRLPP 366							
Db	420	GLLPRQVSANS-BGMNDLIVLTWOPPRKDSDAVQYVVVERELPFGDTPVPLWLRSP 478							
Qy	367	GNLSTLLPGEEKGGVPYRITYTVAYSGGLAAAPSWGFREELVPLLAGPAYWRLPDPPT 426							
Db	479	YNVALISENIKSYTCYEIRYVANL-SGDQGCSSILGNSRKHAPLSGPHINATTE-KGS 536							
Qy	427	PVVAEGVPFHQLRGQATHWTFCTOSRGLSTCVRANSSQTOQTATLP----NLH---- 475							
Db	537	ILKNSNKSIPVQEONGCCLHYRIYNE-----RDNSSQFOLCEIPYRSQNSHIPSINSLQ 589							
Qy	476	-SGSFKLWVWVSTVYAGQGPFPDLSLHLPDRNIRWKALPFLSLWLGCGLSSLASTR 534							
Db	590	PRVYVLWMLALTAGESSIGNERFECFL-GKANWMAFPSCIAIIMVG---IFSTH 644							
Qy	535	CLOARCLHWRKHLKPQWINERPDPANSNSGQPY-IKEYSLQP-----PKDGP! 583							
Db	645	YFQKVFLVLAALRPQWCSEIPDPANSCTAKYPIAEETQPLPDRLLDWPPDPDPEP 704							
Qy	584	LEVEEV--EIQPVYVESPKAS 601							
Db	705	LVISEVLHQVTPVFRHPPCS 724							
RESULT	2								
T112S_MOUSE	ID	T112S_MOUSE	STANDARD;	PRT;	874 AA.				
AC	P97378;								
DT	20-AUG-2001	(Rel. 4.0, Created)							
DT	20-AUG-2001	(Rel. 4.0, Last sequence update)							
DT	20-AUG-2001	(Rel. 10, Last annotation update)							
DE	INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN PRECURSOR	(IL-12 RECEPTOR BETA-							

Query Match 9.9%; Score 339.5; DB 1; Length 874;  
 Best Local Similarity 22.1%; Pred. No. 1.6e-17;  
 Matches 155; Conservative 108; Mismatches 279; Indels 159; Gaps 36;  
 19 M\$LLLGTRPHGS\$GPLQQSYVGLIINC\$W\$P\$LGDL\$ETPPVLYHQSQKYHPNRWEVKV 78

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Result No.	Score	Query	Match	Length	DB	ID	Description
1	3044	100.0	623	11	070394		070394 mus musculus
2	345	59.7	636	4	060624		060624 homo sapiens
3	282	8.2	971	11	070458		070458 bos taurus
4	279.5	8.2	970	11	088821		088821 mus musculus
5	278	8.1	881	13	057519		057519 xenopus laevis
6	277	8.1	710	13	057520		057520 xenopus laevis
7	259	7.6	1093	11	070535		070535 rattus norvegicus
8	243.5	7.1	918	13	Q9W6U9		Q9W6U9 gallus gallus
9	161.5	4.7	622	6	Q9N0J7		Q9N0J7 homo sapiens
10	193.5	5.7	979	4	Q99650		Q99650 homo sapiens
11	167.5	4.9	581	6	Q46561		Q46561 ovis aries
12	165.5	4.8	296	6	Q18880		Q18880 bos taurus
13	164	4.8	1140	4	Q9P218		Q9P218 homo sapiens
14	163	4.8	1207	4	Q9BQU7		Q9BQU7 homo sapiens
15	161.5	4.7	622	6	Q9N0J7		Q9N0J7 callithrix jacchus
16	161	4.7	26926	4	Q10466		Q10466 homo sapiens
17	160.5	4.7	4280	5	Q9UB29		Q9UB29 caenorhabditis elegans
18	160.5	4.7	4450	5	Q9UB28		Q9UB28 mus musculus
19	159	4.6	2944	11	Q63870		Q63870 mus musculus

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5
OM protein - protein search, using sw model	
Run on: May 9, 2002, 06:10:49 ; Search time 50.89 Seconds (without alignments)	1790.679 Million cell updates/sec
Title: US-09-692-504-2	
Perfect score: 3424	
Sequence: 1 MNRLYARLTPLELLSMLS.....IYSGYEKHFPLTPEELGLV 623	
Scoring table: BL005M62	
GapP 10.0 , Gapext 0.5	
Searched: 473505 seqs, 14627329 residues	
Number of hits satisfying chosen parameters:	473505
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	

## ALIGNMENTS

RESULT	1						
070394	ID	070394	PRELIMINARY;	PRT;	623 AA.		
	AC	070394;					
	DT	01-AUG-1998	(TRIMBLrel. 07, Created)				
	DT	01-AUG-1998	(TRIMBLrel. 07, Last sequence update)				
	DT	01-JUN-2001	(TRIMBLrel. 17, Last annotation update)				
	DE	CLASS I CYTOKINE RECEPTOR.					
	GN	WSXL.					
	OS	Mus musculus (Mouse).					
	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
	OX	NCBI_TaxID-10090;					
	RN	[1]					
	RP	SEQUENCE FROM N.A.					
	RX	MEDLINE-#98262921; PubMed=9600072;					
	RA	Sprecher C.A., Grant F.J., Baungartner J.W., Presnell S.R.,					
	RA	Schrader S.K., Yamagawa T., Whitmore T.E., O'Hara P.J., Foster D.F.;					
	RT	*Cloning and characterization of a novel Class I cytokine receptor.					
	RL	Biochem. Biophys. Res. Commun. 246:92-90 (1998).					
	DR	EMLB; AF053005; AAC0121.1; -.					
	DR	MGD; MGI:1355318; Wsxl.					
	DR	Intero; IPR003961; FN_III.					
	DR	SMART; SM00060; FN3; 1.					
	SQ	SEQUENCE 623 AA; 68998 MW; 4 BA20FEC875A7180 CRC64;					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Query	Match	Length	DB	ID	Description
1	3044	100.0	623	11	070394
2	345	59.7	636	4	060624
3	282	8.2	971	11	070458
4	279.5	8.2	970	11	088821
5	278	8.1	881	13	057519
6	277	8.1	710	13	057520
7	259	7.6	1093	11	070535
8	243.5	7.1	918	13	Q9W6U9
9	161.5	4.7	622	6	Q9N0J7
10	193.5	5.7	979	4	Q99650
11	167.5	4.9	581	6	Q46561
12	165.5	4.8	296	6	Q18880
13	164	4.8	1140	4	Q9P218
14	163	4.8	1207	4	Q9BQU7
15	161.5	4.7	622	6	Q9N0J7
16	161	4.7	26926	4	Q10466
17	160.5	4.7	4280	5	Q9UB29
18	160.5	4.7	4450	5	Q9UB28
19	159	4.6	2944	11	Q63870

Query Match Length DB ID Description

070394 mus musculus

060624 homo sapiens

070458 bos taurus

088821 mus musculus

057519 xenopus laevis

057520 xenopus laevis

070535 rattus norvegicus

Q9W6U9 gallus gallus

Q9N0J7 homo sapiens

Q99650 homo sapiens

Q46561 ovis aries

Q18880 bos taurus

Q9P218 homo sapiens

Q9BQU7 homo sapiens

Q9N0J7 calithrix jacchus

Q10466 homo sapiens

Q9UB29 caenorhabditis elegans

Q9UB28 mus musculus

Q63870 mus musculus

Best Local Similarity 100.0%; Pred. No. 1-3e-261; Mismatches 0; Indels 0; Gaps 0;

Query Match Length DB ID Description

1 MNLRVARYTPELELLSMLSILLGPRHGSGLPQCYSYGPGLIUNCSWEPLGDLTEPPV 60

1 MNLRVARYTPELELLSMLSILLGPRHGSGLPQCYSYGPGLIUNCSWEPLGDLTEPPV 60

1 LYHQSKYHPNRVWEKVPKSQSWNTIPREOFTMDKLILLWGTOQGRPLSSVSYNLLETQ 120

1 LYHQSKYHPNRVWEKVPKSQSWNTIPREOFTMDKLILLWGTOQGRPLSSVSYNLLETQ 120

1 MKPDTPQIFSQYDISSEBATLVAPPWPPQKALTQCPRYKEQAEATRLEBPQLKT 180

Query Match		Score 59.7%	Score 2044;	DB 4;	Length 636;
Best Local Similarity	62.8%	Pred. No. 7e-153;	Mismatches 61;	Indels 8;	Gaps 3;
Matches	388;	Conservative	61;		
Query	9	LTPBLLELLSMLSLLGTAPHGSPGLPQOQYSVGPGLIUNCSWBPLGLDLTTPPVLYHQSQKY 68			
SEQUENCE FROM N.A.	1	RT SubMITTED (NOV-1998) to the EMBL/GenBank/DBJ databases.			
RA	1	PMID: 98262921; PubMed=9600072;	RA PMID: 98262921; PubMed=9600072;	RA PMID: 98262921; PubMed=9600072;	RA PMID: 98262921; PubMed=9600072;
RA	2	Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,	RA Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,	RA Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,	RA Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R.,
RA	3	Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;	RA Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;	RA Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;	RA Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;
RA	4	"Cloning and characterization of a novel class I cytokine receptor";	RA "Cloning and characterization of a novel class I cytokine receptor";	RA "Cloning and characterization of a novel class I cytokine receptor";	RA "Cloning and characterization of a novel class I cytokine receptor";
RA	5	Biochem. Biophys. Res. Commun. 246:82-90 (1998).	RA Biochem. Biophys. Res. Commun. 246:82-90 (1998).	RA Biochem. Biophys. Res. Commun. 246:82-90 (1998).	RA Biochem. Biophys. Res. Commun. 246:82-90 (1998).
RA	6	SEQUENCE FROM N.A.	RA SEQUENCE FROM N.A.	RA SEQUENCE FROM N.A.	RA SEQUENCE FROM N.A.
RA	7	Zhang W., Wan T., He L., Yuan Z., Cao X.;	RA Zhang W., Wan T., He L., Yuan Z., Cao X.;	RA Zhang W., Wan T., He L., Yuan Z., Cao X.;	RA Zhang W., Wan T., He L., Yuan Z., Cao X.;
RA	8	"A novel gp130-like cytokine receptor";	RA "A novel gp130-like cytokine receptor";	RA "A novel gp130-like cytokine receptor";	RA "A novel gp130-like cytokine receptor";
RA	9	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR	1	EMBL; AF053004; AAC39755.1; -.	DR EMBL; AF053004; AAC39755.1; -.	DR EMBL; AF053004; AAC39755.1; -.	DR EMBL; AF053004; AAC39755.1; -.
DR	2	InterPro; IPR003961; FN_III.	DR InterPro; IPR003961; FN_III.	DR InterPro; IPR003961; FN_III.	DR InterPro; IPR003961; FN_III.
DR	3	Pfam; PF00041; fn3; 2.	DR Pfam; PF00041; fn3; 2.	DR Pfam; PF00041; fn3; 2.	DR Pfam; PF00041; fn3; 2.
DR	4	SMART; SM00050; FN3; 1.	DR SMART; SM00050; FN3; 1.	DR SMART; SM00050; FN3; 1.	DR SMART; SM00050; FN3; 1.
DR	5	SEQUENCE 636 AA; 69473 MN; DC7DAAABA643CE97 CRC64;	DR SEQUENCE 636 AA; 69473 MN; DC7DAAABA643CE97 CRC64;	DR SEQUENCE 636 AA; 69473 MN; DC7DAAABA643CE97 CRC64;	DR SEQUENCE 636 AA; 69473 MN; DC7DAAABA643CE97 CRC64;
RESULT	2	060624 PRELIMINARY; PRP; 636 AA.			
AC	1	01-AUG-1998 (TREMBLrel. 07, Created)	01-AUG-1998 (TREMBLrel. 07, Last sequence update)	01-AUG-1998 (TREMBLrel. 07, Last annotation update)	01-AUG-1998 (TREMBLrel. 17, Last annotation update)
DT	2	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	3	CLASS I CYTOKINE RECEPTOR (CRL1 PROTEIN).			
OS	4	Homo sapiens (Human).	Homo sapiens (Human).	Homo sapiens (Human).	Homo sapiens (Human).
OC	5	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	6	NCBI_TaxID=9506;	NCBI_TaxID=9506;	NCBI_TaxID=9506;	NCBI_TaxID=9506;
RN	7	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RN	8	PMID: 98262921; PubMed=9600072;	PMID: 98262921; PubMed=9600072;	PMID: 98262921; PubMed=9600072;	PMID: 98262921; PubMed=9600072;
RN	9	Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R., Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;	Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R., Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;	Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R., Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;	Spiecher C.A., Grant F.J., Baumgartner J.W., Presnell S.R., Schraeder S.K., Yamagishi T., Whitmore T.E., O'Hara P.J., Foster D.F.;
RA	10	"Cloning and characterization of a novel class I cytokine receptor"; Biochem. Biophys. Res. Commun. 246:82-90 (1998).	"Cloning and characterization of a novel class I cytokine receptor"; Biochem. Biophys. Res. Commun. 246:82-90 (1998).	"Cloning and characterization of a novel class I cytokine receptor"; Biochem. Biophys. Res. Commun. 246:82-90 (1998).	"Cloning and characterization of a novel class I cytokine receptor"; Biochem. Biophys. Res. Commun. 246:82-90 (1998).
RA	11	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RA	12	Zhang W., Wan T., He L., Yuan Z., Cao X.;	Zhang W., Wan T., He L., Yuan Z., Cao X.;	Zhang W., Wan T., He L., Yuan Z., Cao X.;	Zhang W., Wan T., He L., Yuan Z., Cao X.;
RA	13	"A novel gp130-like cytokine receptor";			
RA	14	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
RC	15	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	16	TISSUE=Lymph Node.	TISSUE=Lymph Node.	TISSUE=Lymph Node.	TISSUE=Lymph Node.
RC	17	Created)	Created)	Created)	Created)
DT	18	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	19	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	20	IL-12 RECEPTOR BETA2 PRECURSOR.			
GN	21	Bos taurus (Bovine).	Bos taurus (Bovine).	Bos taurus (Bovine).	Bos taurus (Bovine).
OC	22	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	23	Bovidae; Bovinae; Bos.	Bovidae; Bovinae; Bos.	Bovidae; Bovinae; Bos.	Bovidae; Bovinae; Bos.
OC	24	NCBITaxID=9513;	NCBITaxID=9513;	NCBITaxID=9513;	NCBITaxID=9513;
RN	25	POTENTIAL.	POTENTIAL.	POTENTIAL.	POTENTIAL.
FT	26	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
FT	27	IL-12 RECEPTOR BETA2.	IL-12 RECEPTOR BETA2.	IL-12 RECEPTOR BETA2.	IL-12 RECEPTOR BETA2.
FT	28	PREDICTED.	PREDICTED.	PREDICTED.	PREDICTED.
FT	29	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	30	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	31	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	32	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	33	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	34	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	35	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	36	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	37	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	38	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	39	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	40	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	41	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	42	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	43	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	44	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	45	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	46	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	47	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	48	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	49	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	50	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	51	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	52	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	53	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	54	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	55	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	56	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	57	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	58	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	59	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	60	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	61	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	62	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	63	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	64	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	65	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	66	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	67	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	68	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	69	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	70	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	71	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	72	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	73	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	100	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	101	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	102	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	144	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	153	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	155	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	159	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	160	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	161	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	169	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	173	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	174	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	179	PRIMER.	PRIMER.	PRIMER.	PRIMER.
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FT	181	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	182	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	183	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT	184	PRIMER.	PRIMER.	PRIMER.	PRIMER.
FT					

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	RESULT	1	
/SIDS8/	cgdata/geneseq/geneseqp/AA1989.DAT : *	AAW33400	
/SIDS8/	cgdata/geneseq/geneseqp/AA1990.DAT : *	ID	AAW33400 standard; Protein; 623 AA.
/SIDS8/	cgdata/geneseq/geneseqp/AA1991.DAT : *	XX	
/SIDS8/	cgdata/geneseq/geneseqp/AA1992.DAT : *	AC	AAW33400;
/SIDS8/	cgdata/geneseq/geneseqp/AA1993.DAT : *	XX	22-MAY-1998 (first entry)
/SIDS8/	cgdata/geneseq/geneseqp/AA1994.DAT : *	DT	Mouse haematopoietic cytokine receptor zcyt01.
/SIDS8/	cgdata/geneseq/geneseqp/AA1995.DAT : *	XX	
/SIDS8/	cgdata/geneseq/geneseqp/AA1996.DAT : *	DE	
/SIDS8/	cgdata/geneseq/geneseqp/AA1997.DAT : *	XX	
/SIDS8/	cgdata/geneseq/geneseqp/AA1998.DAT : *	KW	Mouse; haematopoietic cytokine receptor; Zcyt01; ligand detection; cancer diagnosis; agonist; antagonist; murine.
/SIDS8/	cgdata/geneseq/geneseqp/AA1999.DAT : *	KW	
/SIDS8/	cgdata/geneseq/geneseqp/AA2000.DAT : *		

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

סוד גנוזה

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PB  
19-MAY-1997;

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PR 23-MAY-1996; 96US-0653740.

xx

PA (ZYMO ) ZYMOGENETICS INC.

xx

PI Baumgartner JW, Foster DC,

- xx

DR WPI; 1998-018509/02.

DR N-PSDB; AAT94121;

### PT Haematoxylin cytochrome c

PT pathological condition diagnosis

פְּנֵי יְהוָה כְּבָשָׂר וְלִבָּשָׂר

The present sequence is the mouse haematopoietic cytokine receptor zcytot1, useful for ligand detection, and pathological condition diagnosis, including cancer. Receptor agonists of the protein can be used to stimulate the proliferation and development of target cells in vitro and *in vivo*. The agonists can stimulate cell mediated immunity and lymphocyte proliferation, to treat infection involving immunosuppression, e.g. viral infections. They may also be used to suppress tumours, induce cytotoxicity, treat leukopenias and enhance the regeneration of the T-cell repertoire after bone marrow transplantation. Antagonists of the protein may be used to suppress the immune system, treat autoimmune diseases, including rheumatoid arthritis, multiple sclerosis and diabetes mellitus. Immune suppression caused by the antagonists can also be used to reduce rejection of tissue or organ transplants and grafts, and to treat T-cell specific leukaemias and lymphomas.



The agonists can stimulate cell mediated immunity and lymphocyte proliferation, to treat infection involving immunosuppression, e.g. viral infections. They may also be used to suppress tumours, induce cytotoxicity, treat leukopenias and enhance the regeneration of the T-cell repertoire after bone marrow transplantation.

Antagonists of the protein may be used to suppress the immune system, treat autoimmune diseases, including rheumatoid arthritis, multiple sclerosis and diabetes mellitus. Immune suppression caused by the antagonists can also be used to reduce rejection of tissue or organ transplants and grafts, and to treat T-cell specific leukaemias and lymphomas.

**Sequence 636 AA:**

Query Match	59.7%	Score 2044;	DB 19;	Length 636;	
Best Local Similarity	62.8%	Pred. No. 6.7e-155;			
Matches	388;	Conservative	61;	Mismatches	161;
				Indels	8;
				Gaps	3;
Qy	9	LTPLELLSLMSLLGTRPHGS <sup>p</sup> GPLOCYSVPGPLGLNCMSWPLGDLDETPPVLYHOSQKY	68		
Db	14	lprklalplllwlfqrtrpqssagp <sup>q</sup> cygrgprglncswplgdlgapselhqsqky	73		
Qy	69	HPNRVWEVKVPKSQSHNTIPREQFTNADKLLTWGTOKRGRPLWSSSVNLLETQMKPDTPQI	128		
Db	74	rskntqtqvaavaqrswaipreqltmsdklwwgtagqlwpvfvlnetqmkmphapri	133		
Qy	129	FQYDISEEATLAEATQWAPPWPPQKAFTCQFRKECAFAWTREPEQLKTGDGTPEVM	188		
Db	134	9pdvdteddppleatvhawppwshkvlvcifhyrcqaswtlpeplkitptpvei	193		
Qy	189	QNEPLGTCYQVSRCQCVENGY <sup>p</sup> -WGEMWSPLSFQTPLDPDVWISGTVCTESGKRALL	247		
Db	194	qdeletaqkygrcrtmekeedlwgswpsllfqfppsapkdwwsgnlgctggceepll	253		
Qy	248	WKDPRPRCVQVYTYWFGAGDTTTOEVPCCKSPVPAWMWAVVSPGNSTSWSWPPTNLS	307		
Db	254	1wkapgpvcqsykvwwfgrelspqitccs11psgaewarysvavntswpltnls	313		
Qy	308	IWCCLAPPSAPCVGVSSADGSGIKYTWKQTRKPLIEYYWDQODDSLKLNTRLPPG	367		
Db	314	1vcldssaspravassiaigststelltwqwpgeplhevwdwargdpdleinwrlppg	373		
Qy	368	NLSTLLPGEFKGVPSRITRAVYSGGLAAAPSPSYNGFRELVELVPLGAPAVNRLPDPPGTP	427		
Db	374	nlsallpgnftgvpyritvaasaglasaswngfreelaplvgptlwrlqdappgtlp	433		
Qy	428	VWAGEVPRHQRLGQATHYFCIQSGLSITCRNVSSQTOTATLPNLHSASFKLWVTNST	487		
Db	434	aiaawgevprhqrlghthyticqsgtspsvcmqsgntqsvtlpdwgpcelwvtast	493		
Qy	488	VGQQGPGPDSLHPLPNRTRKALPWFSLWGLLIMGCCGSLASTRCLQARCHEWRHKL	547		
Db	494	iaggqgpqgp1rlrhlpantikrwkvpg1flwg1flwg1flwg1flwg1flwg1flwg1	549		
Qy	548	LFWQINERVPDPDANSNSGQPYKEYSLPQPKDGPTILEVEELQPVVES--PKASAPI	604		
Db	550	1prwwvevpdpansssqqmneqpvpeaqp1qdlpileveemppvmesssqpaqatapl	609		
Qy	605	YSGYEKHFLPTEELGIL	622		
Db	610	dsgyekhflpfeelgil	627		

RESULT 4  
 AAU01853 ID AAU01853 standard; Protein; 636 AA.  
 XX AC AAU01853;  
 XX DT G7-SEP-2001 (first entry)  
 XX DE Human type I cytokine receptor, htCCR1.  
 XX PN WO200129070-A2.  
 XX PD 26-APR-2001.  
 XX PF 18-OCT-2000;  
 XX PR 20-OCT-1999;  
 XX PA (GETH ) GENENTECH INC.

XX	De Sauvage FJ, Grewal I, Gurney AL;	Qy	548 LPQWIWERVPDPANSNSGQPYIKEVSLPOPKDGPILEVEELQPVVES--PKASAPI 604
PI	WPI: 2001-308474/32.	Db	550 1prwrxkyodpanssgpmeypeaqplgdplieeveemppmessoqpgatap1 609
XX	N-PSDB; AAS03262.	Qy	605 YSGYEKHFPLPTEELGL 622
DR		Db	610 dsgyekhfplpceig1l 627
PT	Modulating T-cell differentiation and cytokine release profiles into Th1 and Th2 subtypes, for treating immune-related diseases in mammals, by administering modulator of type I cytokine receptor (TCCR) -	RESULT 5	
PT	Example 1; Fig 3; 126pp; English.	ID	AY29781 standard; Protein; 636 AA.
XX	The sequence represents human type I cytokine receptor, hTCCR. The invention relates to methods of modulating the differentiation of T-cells into the Th2 subtype instead of the Th1 subtype, by administering a modulator of TCCR (e.g. an antagonist) to enhance, stimulate or potentiate T-cell differentiation, or using TCCR polypeptide or its agonists to prevent, inhibit or attenuate T-cell differentiation. Th1 mediated disease in mammal can be treated by administering a TCCR antagonist and Th2 disease by administering a TCCR antagonist. Th1-mediated diseases include allograft rejection and autoimmune inflammatory diseases, such as allergic encephalomyelitis, multiple sclerosis, insulin-dependent diabetes mellitus, uveoretinitis, inflammatory bowel disease or autoimmune thyroid disease. Th2-mediated diseases include infectious diseases, such as Leishmania major, Mycobacterium leprae, Candida albicans, Toxoplasma gondii, respiratory syncytial virus and human immunodeficiency virus (HIV) and allergic disorders, such as asthma, allergic rhinitis, dermatitis and vernal conjunctivitis.	XX	Human DNAX cytokine receptor subunit 1.
XX	Sequence 636 AA;	AC	AY29781;
CC		XX	04-NOV-1999 (first entry)
CC		DE	
CC		XX	DNAx soluble receptor subunit 1; DNAx cytokine receptor; diagnosis;
CC		XX	KW interleukin B30; DRS1; DCRS1; IL-B30; cytokine receptor; innate immunity; inflammatory disorder; inflammatory response; innate immunity; morphogenic development; immunological disorder.
CC		XX	
CC		OS	Homo sapiens.
CC		PN	
CC		XX	Key Location/Qualifiers
CC		FT	Misc-difference 108
CC		FT	/label= "encoded by AYT"
CC		FT	/note= "encoded by AYT"
CC		XX	
SO		PN	W09940195-A1.
SO		XX	
SO		XX	12-AUG-1999.
SO		PD	59.7% Score 2044; DB 22; Length 636;
SO		XX	Best Local Similarity 62.8%; Pred. No. 6.7e-155;
SO		PP	Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;
SO		XX	05-FEB-1999; 99WO-US02600.
Qy	9 LTPLELLSLSMILLGTRPHGSQPLQCYSGVPGILNCWSWEPLGDLTTPPVLYHQSQKY 68	PR	13-MAY-1998; 98US-0078194.
Db	14 lpkallpllwlfqrtpqsgaspqlqcgvqvpqldincswep1gdlgapsehlqsgqy 73	PR	06-FEB-1998; 98US-0073941.
Qy	69 HPNRWEVKVPSKOSWVTPREOPTMDKLILLINGTQGRPLWSSVSVNLETQMKPDTP0I 128	PA	(SCHERING CORP.
Db	74 rsnktqtavavaqrswwalpreq1tsdkllvwgtkqasq1lwwgtvfnalqmkpnapr1 133	XX	
Qy	129 FQVDISATELVQAVAPPVNPQKATTCQFYCAEANTTRLEPLKTQDLPYEM 188	P1	Kastelein RA, Mattson JD, McClanahan TK;
Db	134 qpdvdseedp1eletvhwaptpshkvicqhyrrceaaawllepektipitptrei 193	XX	
Qy	189 QNLEPGTCTQYSGRCQVENGYP-WGEWSSSPSFOTPFELDPEDPVWVSGVCETSGSKRAALL 247	XX	WPI: 1999-527306/44.
Db	194 qdilelatgkvygrormekeed1gewps1sfotpssapkdwvsgn1cgtpqgeep1 253	DR	N-PSDB; AAZ08863.
Qy	248 VRDPRRPCVQYTYYWFQGDDITTQEEVPCCKSPPVPAWMEMAWVSPGNISTSWVPTNLS 307	XX	New receptor subunits useful in the treatment inflammatory disorders
Db	254 1wkappgcvqsj1kwvfwwggrelspgitzccslipsqgaewarvartswepltns 313	XX	Claim 2; Page 14-17; 133pp; English.
Qy	308 NLSTLPLGPGRFKGGPYRTVAYVSGGLAAAPSTWGFREELVLPLAGPAWRLPNDPPCPMP 367	XX	The present invention describes a composition (I) comprising DNAS cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor subunit I (DSRS1) protein, which together encode a new mammalian cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or DSRS1 and IL-B30 proteins (II) comprising DRS1 and DCRS1 is useful for screening for ligands (i.e. agonists/antagonists) from a library of compounds, which are useful for modulating the physiology or development of a cell or tissue culture e.g. inflammatory responses, innate immunity and/or morphogenic development. (R), antibodies and ligands are useful for treatment of conditions, especially immunological disorders, associated with conditions exhibiting abnormal expression of (R). (R) is useful as a phosphate labeling enzyme to label substrates, and the subunits DRS1 and DCRS1 are useful as immunogens for generating antibodies or as antigens for binding antibodies. Nucleic acids encoding (R) are useful for identifying related DNAs and mRNAs, and variants from other individuals or species. The present sequence represents the specifically claimed human DCRS1, for use in the composition of the present invention.
Db	314 1vcldasapsrsvsstagsstel1vtwgpgepleinrvdwardgdpklowvrlp1g 373	XX	
Qy	368 NLSTLPLGPGRFKGGPYRTVAYVSGGLAAAPSTWGFREELVLPLAGPAWRLPNDPPCPMP 427	XX	
Db	374 n1s1lpqntgqpyrltvavasgiaassasywgfreelaplvgptlwrigdappg1p 433	XX	
Qy	428 VVANGEVPRHLRQOATHYFCIOSRLGSTVCRNNSOTATLPLNLSLHSFKLWVTVST 487	XX	
Db	434 a1angevprhlqghlyt1cagqsg1spsvcmnvsqntgsv1lpdpwgpcelwtast 493	XX	
Qy	488 VAGGGPPGFDLSLHLPLDNIRWIRALPWNFLWIRLQASLRCLQARCHHWIRKL 547	XX	
Db	494 1agggppgplrlhpndtirwkvlpgilfligfligcgls1ats---gcyh1rhkv 549	Sequence 636 AA;	

Query Match	59 %;	Score 2036;	DB 20;	Length 636;		xx	Baumgartner JW,	Foster DC,	Grant FJ,	Sprecher CA;
Best Local Similarity	62.5 %;	Pred. No. 2.9e-154;			3;	xx				
Matches 386; Conservative	62;	Mismatches 162;	Indels 8;	Gaps 3;		xx	DR			
						xx	WPI; 1998-018509/02.			
Qy 9 LPLELLSLSMSLLGTRPHSPGLQCVSVGPGLLNCSWEPLPVLHQSQKY	68					xx	N-PSpp;	AAT94119.		
Db 14 Ipkialpllwlfqtrprgsgaplgcqvgvpqglndnswepqgdigapsehlqskqy	73					xx	Haematoopoietic cytokine receptor - useful for ligand detection, and pathological condition diagnosis			
Qy 69 HPNRYWEVKVPSKQSWVTTIREQFTMADKULLWGTQKGRLPLWSSSVNLNETOMKPDTPQI	128					xx	PT			
Db 74 rsnktcqtvavaagsrwvalapregltmsdkllivgxkagqlpwppfvnlletqmhpnaapr1	133					xx	PT			
Db 134 qpdvateddpoleatvhwaptpkhvlicqhyrcgaaatlepeiltptve1	193					xx	PT			
Qy 189 QNLERGTQYQSGRCQVENGYP-MGEWSSPLSFQTPFLDPEVVSGTVCETSGKRAALL	247					xx	PS	Claim 1; Pages 39-43; 86PP; English.		
Db 194 qdletatqkvygrcmekedlqgewspisfqtpsspkdhwvsgnictpggeep11	253					xx	CC	The present sequence is the human haematoopoietic cytokine receptor zcytor1, useful for ligand detection, and pathological condition diagnosis, including cancer. Receptor agonists of the protein can be used to stimulate the proliferation and development of target cells in vitro and in vivo. The agonists can stimulate cell mediated immunity and lymphocyte proliferation, to treat infection involving immunosuppression, e.g. viral infections. They may also be used to suppress tumours, induce cytotoxicity, treat leukoaplasias and enhance the regeneration of the T cell repertoire after bone marrow transplantation. Antagonists of the protein may be used to suppress the immune system, treat autoimmune diseases, including rheumatoid arthritis, multiple sclerosis and diabetes mellitus. Immune suppression caused by the antagonists can also be used to reduce rejection of tissue or organ transplants and grafts, and to treat T-cell specific leukaemias and lymphomas.		
Qy 248 VWDKDRPCVQTVTYWFAGDTITQEEYPCCKSKSPVPMANEWAVVSPGNSTSWSYPTNLNS	307					xx	CC			
Db 254 1wkargpcvcqvsykxwfwgrygrelspqgitccslipsgaewaravsvanswep1thns	313					xx	CC			
Qy 308 LVCLAPESAPCDVGASSADGSPGIKVTKWTGKTRPKLEPYVVDWAQGDSDLKLNWTRLPPG	367					xx	CC			
Db 314 1vcldasaprsrvass1sgstel1tvwgppglehvdwardgdp1ekinuvrlppg	373					xx	CC			
Qy 368 NLSTLLPGERFKGGPYRITYTAVSYGGLAAAPSYWGFFREEFLPLAGPAYNWLPPDPGTP	427					xx	CC			
Db 374 nlsal1pgnttvqpyritvavasqglasasywgfreelapvgptwlriqappgt	433					xx	Sequence	578 AA;		
Qy 428 VVANGEVPRHQLRGATHYFCISQRGLSTVCRNVSQTQATLPNLHGSFKLWVTVST	487					xx	Query	54.5%; Score 1866.5; DB 19; Length 578;		
Db 434 aiawgevpqrhqlrhyltcaisgtspsvcmnysqstvlpdlpgpcelwvtast	493					xx	Match	54.5%; Score 1866.5; DB 19; Length 578;		
Qy 488 VAGQQGPGPDLSLHPDNIRWKALPWFSLWGLLUMGCCSLASTRCLQARLUHWRKHKL	547					xx	Best Local Similarity	54.5%; Score 1866.5; DB 19; Length 578;		
Db 494 iaggqqppgpilrlhlpdntrkwv1pg1flwgif1lgcslats---grychirhkv	549					xx	Matches	54.5%; Score 1866.5; DB 19; Length 578;		
Qy 548 LPQWIVWERVPDANSNGQPYIKVNSLPOPDKGPILEVEELQPVVES--PKASAPI	604					xx	Qy	9 LPLELLSLSMSLLGTRPHSPGPGPLQCVSGPGLTNCWSWPLGLDETPPVLYHOSQKY	68	
Db 550 lprwwwekyvpdpanssggphmedyapeadlgipileveemmppvmesssqpagatapl	609					xx	Db	14 ipkialpllwlfqtrprgsgaplgcqvgvpqglngcwep1qglqgapseihlqskqy	73	
Qy 605 YSGYEKHELPTPEEGLL	622					xx	Qy	99 HPNRYWEVKVPSKQSWVTTIREQFMADKULLWGTQKGRLPLWSSSYVNLNETOMKPDTPQI	128	
Db 610 dsgyskhhf1ptpee1q11	627					xx	Db	74 rsnk1gtqvavaagsrw1a1preql1mskl1lvwgt-kagqpl1wpvv1ynetqmknapr1	133	
RE 6 AAW33398 standard; Protein: 578 AA.						xx	Qy	99 HPNRYWEVKVPSKQSWVTTIREQFMADKULLWGTQKGRLPLWSSSYVNLNETOMKPDTPQI	128	
ID AAW33398						xx	Db	129 FSQDISEATLEAFVQWAPPWQPKQALCQFRYKECQEAWTRLEPKLKTDLTPVEM	188	
AC AAW33398;						xx	Qy	129 FSQDISEATLEAFVQWAPPWQPKQALCQFRYKECQEAWTRLEPKLKTDLTPVEM	188	
DT 22-MAY-1998 (first entry)						xx	Db	134 gpvdvseddpleatvhwappwshkvl1cqfhyrrqeqaaawtlepe1ktip1ptve1	193	
DE Human haematoopoietic cytokine receptor zcytor1.						xx	Qy	189 QNLERGTQYQSGRCQVENGYP-WGEWSSPLSFQTPFLDPEDVWVSYGVTCETSGKRAALL	247	
KW Human; haematoopoietic cytokine receptor; zcytor1; ligand detection; cancer diagnosis; agonist; antagonist.						xx	Db	194 qdletatqkvygrcmekedlqgewspisfqtpsspkdhwvsgn1ctpggeep11	253	
XX						xx	Qy	248 VWKDRPCVQYVTFMFGADITTCQEYVPCCKSPVPAWVAVVSPGNTSTSWWPTNLNS	307	
XX						xx	Db	254 1wkargpcvcqvsykxwfwgrygrelspqgitccslipsgaewaravsvanswep1thns	313	
XX						xx	Qy	308 LVCLAPESAPCDVGASSADGSPGIKVTKWTGKTRPKLEPYVVDWAQGDSDLKLNWTRLPPG	367	
XX						xx	Db	314 lvcdasaprsrvass1sgstel1tvwgppglehvdwardgdp1ekinuvrlppg	373	
XX						xx	Qy	368 NLSTLLPGERFKGGPYRITYTAVSYGGLAAAPSYWGFFREEFLPLAGPAYNWLPPDPGTP	427	
XX						xx	Db	434 aiawgevpqrhqlrhyltcaisgtspvcavsgn1ctpggeep11	493	
XX						xx	Qy	488 VAGQQGPGPDLSLHPDNIRWKALPWFSLWGLLUMGCCSLASTRCLQARLUHWRKHKL	547	
XX						xx	Db	494 iaggqqppgilrlhpdt1rkwv1pg1flwgif1lgcslats---grychirhkv	549	
XX						xx	Qy	548 LPQWIVWERVPDANSNGQPYIKVNSLPOPDKGPILEVEELQPVVES--PKASAPI	604	
XX						xx	Db	550 lprwwwekyvpdpanssggphmedyapeadlgipileveemmppvmesssqpagatapl	609	
XX						xx	Qy	605 YSGYEKHELPTPEEGLL	622	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
RE 6 AAW33398 standard; Protein: 578 AA.						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
ID AAW33398						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
AC AAW33398;						xx	Db	610 dsgyskhhf1ptpee1q11	627	
DT 22-MAY-1998 (first entry)						xx	Db	610 dsgyskhhf1ptpee1q11	627	
DE Human haematoopoietic cytokine receptor zcytor1.						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
KW Human; haematoopoietic cytokine receptor; zcytor1; ligand detection; cancer diagnosis; agonist; antagonist.						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Db	610 dsgyskhhf1ptpee1q11	627	
XX						xx	Qy	610 dsgyskhhf1ptpee1		



CC innate immunity and/or morphogenetic development. (R), antibodies and  
 CC ligands are useful for treatment of conditions, especially immunological  
 CC disorders, associated with conditions exhibiting abnormal expression of  
 CC (R). (R) is useful as a phosphate labelling enzyme to label substrates,  
 CC and the subunits DRS1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids  
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
 CC variants from other individuals or species. The present sequence  
 CC represents the partial mouse DCRS1, given in the present invention.  
 XX Sequence 246 AA;

Query Match	39.28;	Score 1342;	DB 20;	Length 246;
Best Local Similarity	100.0%	Pred. No. 2.3e-99;	Gaps 0;	
Matches 246;	Conservative 0;	Mismatches 0;	Indels 0;	
Qy 378 KGGVPYRITVAVYSSGLAAPSNSVGFFREELVPLGAAWRLDDDPGTPTVVAAGEVPRH 437	Db [REDACTED] 1 kgvgpyritvavysglaapsnsvgffreelvplgaaawrldddpgtptvvaagevprh 60			
Qy 438 QLRGQATHYTFICIOSGLSTVCNRYSSQTATNLHSCSFKLWTVSYAGQCPGPQD 497	Db 61 qirggathtytficqslstvcnryssqtatnlhscsfklwtvsvagqcpgpqd 120			
Qy 498 LSHLHPDNRTRKALPWFSLWGLLIMGCCISLASTRCLQARCLHWRHKULLPKWIWERVP 557	Db 121 lshlhpdnrtirkalpwfslwglliclasstrclqarclhwrhkullpkwiwervp 180			
Qy 558 DPANSNSGQPYKTKENSLQPQPKDPILEVEELOPVVESPKASAPIYSGKEKHFLLPTPE 617	Db 181 dpansnsqpyktkenqlqpqpkdpileveevelqvvespkasapiyssyekhfllptpe 240			
Qy 618 EIGLGLV 623	Db 241 e1g1ly 246			

RESULT 9  
 AAY29782 ID AAY29782 standard; Protein: 150 AA.  
 XX AC AAY29782;  
 XX DT 04-NOV-1999 (first entry)  
 XX DE Mouse DNAX cytokine receptor subunit 1.  
 XX KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 KW Interleukin B30; DRS1; DCRS1; IL-B30; Cytokine receptor; diagnosis;  
 KW inflammatory disorder; inflammatory response; innate immunity;  
 KW morphogenetic development; immunological disorder.  
 OS Mus sp.  
 FH XX Key Location/Qualifiers  
 FT Misc-difference 150  
 FT /label= unknown  
 FT /note= "encoded by GAN"  
 XX PN W09940195-A1.  
 XX PD 12-AUG-1999.  
 XX PF 05-FEB-1999; 99WO-US02600.  
 XX PR 13-MAY-1998; 98US-0078194.  
 PR 06-FEB-1998; 98US-0073941.  
 XX PA (SCHE ) SCHERING CORP.  
 XX PI Kastelein RA, Mattson JD, McClanahan TK;  
 XX PT

DR WPI; 1999-527306/44.  
 DR N-PSDB; AA208864.

XX PT New receptor subunits useful in the treatment inflammatory disorders  
 XX PS Claim 2; Page 17-18; 133pp; English.

XX The present invention describes composition (I) comprising DNA  
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 CC subunit I (DSRS1) protein, which together encode a new mammalian  
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
 CC proteins, or DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1  
 CC is useful for screening for ligands (i.e. agonists/antagonists) from  
 CC a library of compounds, which are useful for modulating the physiology  
 CC or development of a cell or tissue culture e.g. inflammatory responses,  
 CC innate immunity and/or morphogenetic development. (R), antibodies and  
 CC ligands are useful for treatment of conditions, especially immunological  
 CC disorders, associated with conditions exhibiting abnormal expression of  
 CC (R). (R) is useful as a phosphate labelling enzyme to label substrates,  
 CC and the subunits DRS1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids  
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
 CC variants from other individuals or species. The present sequence  
 CC represents the specifically claimed mouse DCRS1, for use in the  
 XX composition of the present invention.

SQ Sequence 150 AA;

Query Match	20.88;	Score 712;	DB 20;	Length 150;
Best Local Similarity	98.5%	Pred. No. 2.7e-49;		
Matches 133;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy 1 MNRLRVARLTPIELLSLILGTLTGHPSRPLQLCYSVGPGLILNSWEPICDLETPV 60	Db 15 mnrlgfarltpleilslisllgtphgsplqlcysvgplilnswepicdletpv 74			
Qy 61 LYHQSKYKHPNRPWVEKVPKSKOSWWTIPREDFTMAKLILNGTQKGRLPNSVSVNLTQ 120	Db 75 lyhqskqykhpnrvewkvpskgswtqpreqftmadklliwgtqkgrlwssvsvnltq 134			
Qy 121 MKPDTPOIFSQVDIS 135	Db 135 mkpdtpqifsqvdis 149			

RESULT 10

AAW12771 ID AAW12771 standard; Protein: 862 AA.  
 XX AC AAW12771;

XX DT 12-MAY-1997 (first entry)  
 XX KW Human interleukin-12 beta-2 receptor.  
 KW DE Interleukin-12 beta-2 receptor; IL-12; autoimmune disease;  
 KW multiple sclerosis.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT FT Peptide  
 FT /label= sig-peptide  
 FT Domain  
 FT /label= Extracellular\_domain  
 FT Domain  
 FT /label= 623..646  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT Region  
 FT /label= Cytoplasmic\_tail  
 FT /label= Cytokine\_receptor\_motif

/note= "cytokine receptor superfamily motif  
(cys132..Cys413IW)"

Region 309 309

/label= Cytokine\_receptor\_motif  
(W305SKWS)

Modified-site 47..50

Modified-site /label= N-linked\_glycosylation\_site  
129..131

Modified-site /label= N-linked\_glycosylation\_site  
166..168

Modified-site /label= N-linked\_glycosylation\_site  
186..188

Modified-site /label= N-linked\_glycosylation\_site  
195..197

Modified-site /label= N-linked\_glycosylation\_site  
271..273

Modified-site /label= N-linked\_glycosylation\_site  
347..349

Modified-site /label= N-linked\_glycosylation\_site  
376..378

Modified-site /label= N-linked\_glycosylation\_site  
480..482

Region 667..669

/label= Conserved\_box\_motif  
/note= "conserved motif of cytokine receptor  
superfamily"

Region 699..704

/label= Conserved\_box\_motif  
/note= "conserved motif of cytokine receptor  
superfamily"

Region 786..798

/label= Conserved\_box\_motif  
/note= "conserved motif of cytokine receptor  
superfamily"

XX EP759466-A2.

PD 26-FEB-1997.

XX 23-JUL-1996; 96EP-0111807.

XX 30-MAY-1996; 96US-0018674.

PR 01-AUG-1995; 95US-0001701.

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX Pgubler UR, Presky DH;

DR WPI: 1997-147515/14.

XX New interleukin-12 beta-2 receptor and high binding affinity complexes - have a high affinity for interleukin-12, and are used to treat autoimmune diseases

XX Claim 3; Page 24-29; 53pp; English.

XX New human interleukin-12 (IL-12) receptor beta-2 receptor (AAW12771) has a low binding affinity for IL-12, but when complexed with an IL-12 beta-1 receptor (see also AAW12772), forms a complex with a high binding affinity for IL-12. Its amino acid sequence was deduced from a composite cDNA sequence (AAW59731) obtained from human lymphoblasts. IL-12 receptor beta-2 can be expressed on the surface of transformed host cells, and, as a complex with co-expressed IL-12 receptor beta-1, and used in therapeutic compositions. pref. with at least 1 cytokine antagonist, to treat autoimmune dysfunctions such as rheumatoid arthritis, inflammatory bowel disease and multiple sclerosis. The receptor protein or complex can also be used to detect (ant)agonists of IL-12 activity.

Sequence 862 AA;

Query	Match	Score	DB	Length
QY	5 RVARLTPELLLSLMSLIGLTRPHGSGPLQLCYSVGPGLNCSWERPLGD - LETPPVLY	11.2%	384:	18; Pred. No. 4.9e-22;
Db	102 klacinsdeleiqcgaefvqape-rgnlsckqsgggactwgrdthlyt1q	Best Local Similarity	140;	Gaps 33;
QY	63 HQSQKVKHPNRVWEVK -	88; Mismatches	171;	Conservative Matches
Db	161 lsqpk --ntlwqkqckdiydcyldfginlpe-----pesnfktav-----n	102	klacinsdeleiqcgaefvqape-rgnlsckqsgggactwgrdthlyt1q	160
QY	108 PLWSSVSVNLLETQMKPPTPQIFSQVNDISEATLEATYWQAWAPPWPP ---OKA-----	107	VPSKQSKVNTIPREQFTMDKLILIWGQTQGR	107
Db	205 slgssssl-----pstftfdi-----vrplpp-wdr1rkfqkasvssctl	108	PLWSSVSVNLLETQMKPPTPQIFSQVNDISEATLEATYWQAWAPPWPP ---OKA-----	156
QY	157 -----LTCQFRYKECQADAWTRLEPOLKTDGLTPEVMQNLEPCY --QVSGRCQVE	244	271	273
Db	245 ywrdegllvllrlyrprnsnlwnmn--virkakqghdilakptfeqfisskhly	245	271	273
QY	207 NGYPNGEWSSPLSFQTFPLDPE --DWVSGTVCETSGKRAALLWK -- DPRPOV --	256	347..349	376..378
Db	302 kg-swdssestraqpeeeptgmidwymkrhidsrqqislf-whlnsvearqkikh	302	376..378	376..378
QY	257 -QVTITVWFAGDITTTQEYPCCKSFPVANMEAV -VSPGNSTSWYPPTNLSL -- VCLA	312	376..378	376..378
Db	360 yqvttlqeitgskamtcnitghtswtvtiprtgnavarava-saantskgssalptrnimica	360	376..378	376..378
QY	313 PESAPCDVGSSADGSPIKTYWKQGTRKP --LEYVDWAQ -- DGDSDLKLNNTRLPP	366	376..378	376..378
Db	420 gillaprqvsas-egmdnivltwqppkdpsavgevverwlehpqndtgypinwrsrp	420	376..378	376..378
QY	367 GNLSTLPGERKGGVPRITYAVSGGLAAAPSUNGFREEYLPLAGPAVWRLPDDPGT	426	376..378	376..378
Db	479 ynvsaileenksyicyeiryal-sqdqgqccsllqnskhanapisphinaitee-kgs	479	376..378	376..378
QY	427 PVVANGEVPRHQLRGQATHTFCIQSRGLSTPVCRNVSQTOTATLP -----NLH-----	475	376..378	376..378
Db	537 illiswnsipyrqeqmgclhyriwyke-----rdnsnqpalcipyrvsgnsnshipins1q	537	376..378	376..378
QY	476 -SGSFKLWVTVSTVAQGPPGPDLSLHLPDNRIRMAKLPNWLSLNCGLSLASTR	534	376..378	376..378
Db	590 prtvtylwmaltaaesshnerefc1-gpkanymafva-psicliaimg----isth	590	376..378	376..378
QY	535 CLQARCLHWKRHKLLPKWNIWTPVDPANSNSQPY -IKEVSLPQP -----PKDGP1	583	376..378	376..378
Db	645 yfqqqkvflviaalrpwicseipdpansctckytaektkplidrlldwptpedpep	645	376..378	376..378
QY	584 LEVEEV -ELOPVVESPKAS	601	376..378	376..378
Db	705 lvisev1hqvtpvfrhpcsv	724	376..378	376..378

RESULT 11

AAR25068 standard; Protein; 1001 AA.

ID XX

AC XX

DT 05-JAN-1993 (first entry)

DE hLIF-R.

KW Plasma membrane; transduction; cachexia; hepatocytes; neurons; leukocytes.

XX Homo sapiens.

XX Key Peptide

FT Location/Qualifiers

FT 1..44

FT /label= signal\_peptide

FT	Protein	45..1001	Mature_peptide	
XX				
PN	W09210370-A.			
XX	25-JUN-1992.			
PD				
XX	05-DEC-1991;	91WO-US09112.		
XX	PR 13-DEC-1990;	90US-0626725.		
XX	PR 13-MAR-1991;	91US-0670608.		
PA	(IMMV ) IMMUNEX CORP.			
XX				
PJ	Beckmann MP,	Gearing DP;		
XX				
DR	WPI; 1992-234626/28.			
DR	N-PSDB; AAQ25795.			
XX				
PT	[REDACTED] new leukaemia inhibitory factor receptor proteins - for treating LIF-dependent leukaemia, lipoprotein, bone and calcium metabolism defects e.g. atherosclerosis, obesity etc.			
XX				
PS	Disclosure; Page 28-32; 49pp; English.			
XX				
CC	The sequence given is a leukaemia inhibitory factor (LIF)-receptor (LIF-R). LIF-R proteins are present on the surface of various hematopoietic and non-hematopoietic cells. They are capable of binding LIF molecules. They are mammalian plasma membrane proteins and play an important role in transducing the signal provided by LIF to a cell. This protein has a molecular weight of approx. 190,000 kD. LIF-R proteins can be used to competitively bind LIF and thereby inhibit its binding to cell surface receptors. Soluble LIF-R may be used in therapy to inhibit the effects of LIF induced cachexia in cancer patients to treat lipoprotein metabolism defects such as atherosclerosis and obesity. It may also be useful in the treatment of disorders of bone and calcium metabolism or disorders associated with LIF overproduction associated with hepatocytes, neurons and leukocytes.			
CC				
CC	Sequence 1001 AA;			
SQ				
Query Match	8.2%	Score 280; DB 13; Length 1001;		
Best Local Similarity	21.5%	Pred. No. 1.2e-13;		
Matches	142; Conservative 110; Mismatches 264; Indels 144; Gaps 35;			
Oy	27 PHGSPGPQLQYSGVPGILNCWEP----LGDLTTPYLHQ-SQKYHPNRMVEVKVP 79			
Db	332 ppdtppqinc-ethalkeipicwprrtalvqpratsylvestskyy-vrlikraeap 388			
Oy	80 SKQSW---VTPREQ---FIMADKLIWIGQKGRFL--WSSVSVNLQEMKDPDQPQIF 129			
Db	389 tnesyql1fqmlpngenyftl-----nahmplgrsqstilvnitekyphptsf 439			
Oy	130 SQDISEEATLEATYQWAPPWPPQKALTCQFYKECQAETAWTRLEPQLKTDGILRP--- 185			
Db	440 kvkdnista---vkiswhlpnfakinfleiksns---vqgeqrnvlkgvnsy1 493			
Oy	186 VEMONLEPGCTCYQVSRCQYENGYPMGEWSSPLSQTQTPFLDE--DVWVSGTVCETSKG 242			
Db	494 valdkinpyltlyfrircstefvkwswnkqhlteaspkskgpdtdw----rewssd 548			
Oy	243 RAALLWWKDPRPCVQ----VTTWFGAGDITIQQEEVPCPKSPVPAWNE----WAVV 292			
Db	549 gknlliyskplpineangkilsyivncssdetqslseidpqhkaqirldkndyiisvv 608			
Oy	293 SPGNSTSWPPTNLNSLVCLAPESAPCDVGYSADD-SPGIKVTKQGTRKPLEYVDAWQ 351			
Db	609 ak-nsvgssspksia---smelphmdlkileqqvvnmgkgilltwydpmtcdyikwsn 663			
Oy	352 DGDSDLKL-NRTRLPGCNLSTLPG-EFKGVYPYRTVTAVYSGGLAAAPSVMGFREELY 409			



/note= "Potential N-linked glycosylation site."

XX US5284755-A.

XX 08-FEB-1994.

XX 13-DEC-1990; 90US-0626725.

XX 13-DEC-1990; 90US-0626725.

PR 13-MAR-1991; 91US-0670608.

PR 11-SEP-1992; 92US-0943843.

XX (IMMUNEX CORP.

XX Beckmann MP, Gearing DP;

PR DR; 1994-056341/07.

DR N-PSDB: AAQ55942.

XX PT DNA encoding leukaemia inhibitory factor receptor - esp. soluble protein receptor, used as competitive inhibitor of LIF binding to cell surface, in therapy, diagnosis and assays

XX PS: Figure 2; 44pp; English.

XX CC Soluble forms of the leukaemia inhibitory factor receptor (LIF-R) having the transmembrane domain deleted can be used in therapy, diagnosis, in assays for LIF or LIFR, or for raising antibodies to LIFR. Soluble LIFR proteins can be used for competitive inhibition of binding of LIF to cell surface receptors. Conditions which could benefit from such inhibition include LIF-induced cachexia in cancer patients and lipoprotein metabolism disorders such as atherosclerosis and obesity. Soluble LIFR is also useful in the treatment of disorders of bone and calcium metabolism as well as those associated with the over production of LIF in e.g. hepatocytes, neurons and leukocytes. This clone comprises the full length human LIFR.

XX SQ Sequence 1097 AA;

Query Match 8.1%; Score 277; DB 15; Length 1097;  
Best Local Similarity 21.7%; Pred. No. 2.5e-13;  
Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

Dr 332 pdtpqinc-ethdikeitcswngprvtalvgpratsytlvfsgky-vrirkraeap 388

Qy 80 SKOSW---VTPREQ---FMDADKLIWGTQKGRL---WSVSYNNLETOMKPDTPQIF 129

Db 389 tnesyglifqmplngqnyfl-----nahplgrsqstilvnitekvphyptsf 439

Qy 130 SVDISEATLEATYQWAPPWWPFQKALTQFYREKQAAWTRLEPQLKTGDLTP--- 185

Db 440 kvkdninsta---vkviswhlgnfakinfceielkksns---vqegrnrtikgvessyl 493

Qy 186 VEMQDNPGTQYQSVRCQYENGYPMGEWSSLPSLTQFPFLDE--- 242

Db 494 valdknpytlytfircstetfkwskswnkqhlteaspkspdtwrews---sdgk 550

Qy 243 RAALLYWKDPRPCVQ-----VTTYMFAGDITIQQEVYPCCKSPVPMHE----WAVV 292

Db 551 n-11yw-k-pipineangkisynqscsddetqsiuseidpqhaeairidkndyliisvv 608

Qy 293 SPGNSTSWPPPTNLISLVCLAPESAyCDVGSSADG-SPGIKVTWQGTRKPLEYVWDWAQ 351

Db 609 ak---navgspqskia---smepnndlqkllteqqvymqkgqlltwyhdpmtdvkwcn 663

Qy 352 DGDSDLKL-NWTRLRPPGNLSTLLP-EFRKGVPYRITVAVSGIAAAPS梧GREENLY 409

Db 664 srsrpclmdwkrvpnsnstetviesdefrpgirynfflycrngqyqlrsmyieela 723

Qy 410 PLAGPAWRLPDDPPGTPPVVAVGEVPRHQLRGQATHYTF-----C10SRGGLS 456

Db 724 pivapn-ftvedtsaidsivewdeipeveylfgkgerdtkskmrvlesgrsd 782

Qy 457 TVCRNVSSTQ-TATOPNLH-SGSFEKLWVTVSTVAGGPPGPDLSHL--PDNRIRWKAL 512

Db 783 ikvknidcsgktlrriadlgktsynlvrlayt---dgvgpeksnvvvtkensv---- 834

Qy 513 PWFLSLWGLL-----LMGCGLSLASTRCLOARCHWHRHKLJPONIWER---VP 557

Db 835 -----gltailipavaavivgv---vtsilcytr-----ewketcypdp 874

Qy 558 DPANSNS-----GQYIKEVSL-POPPKDGPFILE-----VEEVE-LQPVVYESPK 599

Db 875 npencahlfqkvscegsaaktlennpcpnvveletsrafplkledelispverpe 934

RESULT 14

AAR74097

ID AAR74097 standard; Protein; 1097 AA.

XX XX AC AAR74097;

XX DT 22-JAN-1996 (first entry)

XX DE Human leukaemia inhibitory factor receptor (LIF-R).

XX KW Leukaemia inhibitory factor receptor; LIF-R; cachexia; human; murine; atherosclerosis; obesity; bone disorder.

XX OS Homo sapiens.

XX PH Location/Qualifiers

FT Key 1..44

FT Peptide /note= "signal peptide"

FT Protein 45..1097 /note= "mature protein - claim 1"

FT Modified-site 64 /note= "glycosylation site"

FT Modified-site 85 /note= "glycosylation site"

FT Modified-site 131 /note= "glycosylation site"

FT Modified-site 143 /note= "glycosylation site"

FT Modified-site 191 /note= "glycosylation site"

FT Modified-site 243 /note= "glycosylation site"

FT Modified-site 303 /note= "glycosylation site"

FT Modified-site 390 /note= "glycosylation site"

FT Modified-site 407 /note= "glycosylation site"

FT Modified-site 426 /note= "glycosylation site"

FT Modified-site 445 /note= "glycosylation site"

FT Modified-site 481 /note= "glycosylation site"

FT Modified-site 489 /note= "glycosylation site"

FT Modified-site 572 /note= "glycosylation site"

FT Modified-site 652 /note= "glycosylation site"

FT Modified-site 663 /note= "glycosylation site"

FT Modified-site 680 /note= "glycosylation site"

FT Misc-difference 689 /note= "glycosylation site"

FT /note= "encoded by CAT"



CC patients and lipoprotein metabolism disorders such as  
 CC atherosclerosis and obesity. Soluble LIFR is also useful in the  
 CC treatment of disorders of bone and calcium metabolism as well as  
 CC those associated with the over production of LIF in e.g.  
 CC hepatocytes, neurons and leukocytes. The LIFR clone 65 is a 5'  
 CC fragment lacking the 3' end.

XX Sequence 1001 AA:

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Query Match          8.1%;  Score 276;  DB 15;  Length 1001;
Best Local Similarity 21.7;  Pred. No. 2.6e-13;
Matches 143;  Conservative 110;  Mismatches 263;  Indels 144;  Gaps 37;
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Db  332 pdtpqglnc-ethdlkeiesswnprvtalvgpratslyesrgky--vrirraeap 388
Qy  80 SKOSW---VTPREQ---FMDADKLIIWGTMKGRLP---WSVSVNLLETQMKPDTPOQIF 129
Dl  389 tnesyqllfqmlpnqeiyntf-----nahuplqrsqsttilvnlitevyphtptsf 439
Qy  130 SQDISEATLEATIVOWAPPWPPQKALTFCRKYECQAETWRLPQLKTDFLP---- 185
Db  440 kvkdnsta---vkiswhlpnafakinfleieirkns---vqegrnvtikgvessyl 493
Qy  186 VEMQNLEPGTCYQVSGRCQVNGCYPGEWSSLSEOTPFELDP---DVWVSGTVCECTSGK 242
Db  494 valdkknpytlfirrcstfwkxkswnmkqlttespskspdtwews---sdgk 550
Qy  243 RAALLYWKDPRPCVQ----VYTYYWFGAGDTTTQEYVPCCKSPVPAWME-----WAVV 292
Db  551 n-lilywk-pplinesngk1syynccssdetqsielpdphkaeiridkndylvsvv 608
Qy  293 SPGNSTSWSWPPTNLSVCLADESAPCDVGYSADG-SPGIKVTKWQGTRKPLEYVVDWAQ 351
Db  609 ak-nsyrgssspskia---smeipnddikleqvvymgkglltwydpmtcdyyikwcn 663
Qy  352 DGDSDLKL-NWTRLPQGNLSTLPG-EFKGEVPYRITVTAVYSGGLAAAPSVWGFREELV 409
Db  664 serspcclmdrkvpnsnteviesdefrgiryfflycrgcqgyql1smigyeela 723
Qy  410 PLAGPAWWRLPDPGTPVVAPEYVRHOLRGQATHYTF-----CIOSRGLS 456
Db  724 pivapn-ftvedtsadsilivkivedpveeifrlgrylfyfgkgerdtshmrvisgrsd 782
Qy  457 TVERNNYSSOTQ-TATLPLNLH-SGSFLKLUWTVTVAQOGPPGPDLISHL - PDNRIRWKAL 512
Dl  783 ikvnknitdisqtktriaqlgkqtsvhvray---dggygpexmyvvtkensv----- 834
Qy  513 PWFLSLNGLL-----LMGCCLSLSAISTRCLQARCLHWRHKLLPQWITWER---VP 557
Db  835 -----glliaillpvavavivjy---vcsilcykr-----ewketfypdip 874
Qy  558 DPANSNS-----GQPYIKEVSL-PQPDKGPILE-----VEEVE-LQPVVESPK 599
Db  875 npenchalqfqgkvscegssalktlemppctpnveletrsafpkiedteispraerpe 934

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Search completed: May 9, 2002, 06:06:16  
 Job time: 148 sec

GenCore version 4.5  
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**protein - protein search, using sw model**

on: May 9, 2002, 06:04:24 ; Search time 24.01 Seconds  
(without alignments)  
583.905 Million cell updates/sec

title: US-09-692-504-2  
effect score: 3424  
Sequence: 1 MNRVARYRATLPLELLSMLS.....IYSGYEKHFLLPPEELGLLV 623

oring table: BloSUM62  
Gapop 10.0 , Gapext 0.5  
searched: 212252 seqs, 22503292 residues

number of hits satisfying chosen parameters: 212252

minimum DB seq length: 0  
maximum DB seq length: 200000000

st-processing: Minimum Match 0<sup>8</sup>  
Maximum Match 100<sup>8</sup>  
Listing first 4 summaries

database : Issued\_Patents\_AA:<sup>\*</sup>

- 1: /cgn2\_6/pidata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/pidata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/pidata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/pidata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/pidata/2/1aa/PCNUS\_COMB.pep:\*
- 6: /cgn2\_6/pidata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

built No.	Score	Query	Match	Length	DB ID	Description
1	3424	100.0	623	1	US-08-653-740-7	Sequence 7, Appli
2	3424	100.0	623	2	US-09-073-594-7	Sequence 7, Appli
3	3424	100.0	623	3	US-09-075-595-7	Sequence 5, Appli
4	2044	59.7	636	1	US-08-653-740-5	Sequence 5, Appli
5	2044	59.7	636	2	US-09-073-594-5	Sequence 5, Appli
6	1866.5	54.5	578	1	US-08-653-740-3	Sequence 3, Appli
7	1866.5	54.5	578	2	US-09-073-594-3	Sequence 3, Appli
8	1866.5	54.5	578	3	US-09-072-595-3	Sequence 3, Appli
9	1866.5	54.5	578	4	US-09-072-595-3	Sequence 2, Appli
10	384	11.2	862	2	US-08-685-118-2	Sequence 2, Appli
11	384	11.2	862	2	US-08-215-195-2	Sequence 2, Appli
12	384	11.2	862	2	US-08-914-530-2	Sequence 2, Appli
13	277	8.1	620	2	US-08-619-650-2	Sequence 7, Appli
14	277	8.1	1001	1	US-07-197-516-6	Sequence 6, Appli
15	277	8.1	1001	1	US-07-943-843-2	Sequence 2, Appli
16	277	8.1	1001	1	US-08-247-003-2	Sequence 2, Appli
17	277	8.1	1097	1	US-08-347-003-6	Sequence 6, Appli
18	277	8.1	1097	1	US-08-347-003-6	Sequence 6, Appli
19	270	7.9	708	1	US-07-797-536-2	Sequence 2, Appli
20	270	7.9	708	1	US-08-308-881-2	Sequence 2, Appli
21	270	7.9	708	2	US-09-058-263-2	Sequence 2, Appli
22	270	7.9	708	2	US-09-059-059-2	Sequence 2, Appli
23	270	7.9	708	3	US-09-058-264-2	Sequence 2, Appli
24	270	7.9	708	5	PCT-US55-06530-2	Sequence 2, Appli
25	264	7.7	918	2	US-08-925-558-6	Sequence 6, Appli
26	261	7.6	602	0	US-08-119-652-6	Sequence 6, Appli
27	261	7.6	783	6	542248-2	Patent No. 542248

**ALIGNMENTS**

RESULT 1  
US-08-653-740-7  
Sequence 7, Application US/08653740  
; Patent No. 5792850  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/653,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 623 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-653-740-7

Query Match 100.0%; Score 3424; DB 1; Length 623;  
Best Local Similarity 100.0%; Pred. No. 3e-292;  
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 MNRQVARLTPLLELLSMLSLLGTRPGSGPLOGYSYGPGLIUNCSWEPGLDGLETPPV 60  
Dn 1 MNPRQVARLTPLLELLSMLSLLGTRPGSGPLOGYSYGPGLIUNCSWEPGLDGLETPPV 60

Qy 61 LYHQSKQYHNPNVWEVKVPSKQSWNTIPREQFTMADKLLIWGTQKRPLASSVSYNLETQ 120  
 Db 61 LYHQSKQYHNPNVWEVKVPSKQSWNTIPREQFTMADKLЛИWGTQKRPLASSVSYNLETQ 120  
 Qy 121 MKPDTPOISQVDISEATLEATVQWAPPWPKQAKALTQCFRYKECQEAETWRLEFOLKT 180  
 Db 121 MKPDTPOISQVDISEATLEATVQWAPPWPKQAKALTQCFRYKECQEAETWRLEFOLKT 180  
 MOLECULE TYPE: protein  
 US-09-073-594-7

Query Match Score 3424; DB 2;  
 Best Local Similarity 100.0%; Pred. No. 3e-292;  
 Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNRLRVARYLTPDELLSLMSLLGTRPHGSQPLQCYSGVPGILNCSWEPLGDLTPTPV 60  
 Db 1 MNRLRVARYLTPDELLSLMSLLGTRPHGSQPLQCYSGVPGILNCSWEPLGDLTPTPV 60

Qy 61 LYHOSQYHNPNVWEVKVPSKOSWNTIPREQFTMADKLILIWTOKSRPLASSVSYNLETQ 120  
 Db 61 LYHOSQYHNPNVWEVKVPSQSWNTIPREQFTMADKLILIWTOKSRPLASSVSYNLETQ 120

Qy 121 MKPDTPOISQVDISEATLEATVQWAPPWPKQAKALTQCFRYKECQEAETWRLEFOLKT 180  
 Db 121 MKPDTPOISQVDISEATLEATVQWAPPWPKQAKALTQCFRYKECQEAETWRLEFOLKT 180

Qy 121 DGLTPVEMQNLSTLPGFHKGGPYRITVTAYSGLAAAPSWMGFEELVPLAGPAWRLP 420  
 Db 121 DGLTPVEMQNLSTLPGFHKGGPYRITVTAYSGLAAAPSWMGFEELVPLAGPAWRLP 420

Qy 121 DPPGTPVVANGEVPRHQLRQAQATHYTFCTQSRGLSTVCRNNSQQTATLPNLHSGSK 480  
 Db 121 DPPGTPVVANGEVPRHQLRQAQATHYTFCTQSRGLSTVCRNNSQQTATLPNLHSGSK 480

Qy 481 LWTVTSTVAGOGPPGFDLSLHPDNIRWKALPWFSLWGLLMLMCGSLSLASTRCIQCRC 540  
 Db 481 LWTVTSTVAGOGPPGFDLSLHPDNIRWKALPWFSLWGLLMLMCGSLSLASTRCIQCRC 540

Qy 541 LHWRKHLLPQIWERTWPDPANSNSGPYIKEVSLOPPKGPILEVEEYLQPVVESPKA 600  
 Db 541 LHWRKHLLPQIWERTWPDPANSNSGPYIKEVSLOPPKGPILEVEEYLQPVVESPKA 600

Qy 601 SAPIVSGYEKHFLPTEPEGLLV 623  
 Db 601 SAPIVSGYEKHFLPTEPEGLLV 623

RESULT 2  
 US-09-073-594-7  
 ; Sequence 7, Application US/09073594  
 ; Patent No. 595735

GENERAL INFORMATION:  
 APPLICANT: James W. Baumgartner  
 APPLICANT: Donald C. Foster  
 APPLICANT: Frank J. Grant  
 APPLICANT: Cindy A. Sprecher  
 TITLE OF INVENTION: HEMATOPOETIC CYTOKINE RECEPTOR  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy diskible  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/073,594  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parker, Gary E  
 REGISTRATION NUMBER: 31,648  
 REFERENCE/DOCKET NUMBER: 95-31

RESULT 3  
 US-09-275-925-7  
 ; Sequence 7, Application US/09275925  
 ; Patent No. 6080406  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James W. Baumgartner  
 ; APPLICANT: Donald C. Foster  
 ; APPLICANT: Frank J. Grant  
 ; APPLICANT: Cindy A. Sprecher  
 ; TITLE OF INVENTION: HEMATOPOETIC CYTOKINE RECEPTOR  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.  
 CITY: Seattle Avenue East  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0,  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/275,925  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parker, Gary E  
 REGISTRATION NUMBER: 31,648  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 623 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-275,925-7

Query Match 100.0%; Score 3424; DB 3; Length 623;  
 Best Local Similarity 100.0%; Pred. No. 3e-222;  
 Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNRLVARLTLLELLSMLSLGTRPHGSPGLCYSVPLGILNCSWEPGLDLETTPV 60  
 Db 1 MNRLVARLTLLELLSMLSLGTRPHGSPGLCYSVPLGILNCSWEPGLDLETTPV 60

Qy 61 LYHQSQKYHPRWVKPSKQSWTIPIRQFTMADKLJLWGTGRPLMSVSYNLLETQ 120  
 Db 61 LYHQSQKYHPRWVKPSKQSWTIPIRQFTMADKLJLWGTGRPLMSVSYNLLETQ 120

Qy 121 MKPDPQIIFSDVSDISSEATLAEATVQAPPWPPQALTCOFRYKECQAEMWTRLEPQLKT 180  
 Db 121 MKPDPQIIFSDVSDISSEATLAEATVQAPPWPPQALTCOFRYKECQAEMWTRLEPQLKT 180

Qy 181 DGLTPYEMONLQEPGTCYQVSRCQVENGYPGENSSPLSFOTPLDPDWGSTVCETS 240  
 Db 181 DGLTPYEMONLQEPGTCYQVSRCQVENGYPGENSSPLSFOTPLDPDWGSTVCETS 240

Qy 241 GKRAILLWWDPRPCVQVTTWFAAGDTTQEIVPCCKSPPAWMENAVSPNSTW 300  
 Db 241 GKRAILLWWDPRPCVQVTTWFAAGDTTQEIVPCCKSPPAWMENAVSPNSTW 300

Qy 301 VPPTNLSLYCLAPESA PCDGVGSADGSP1KVTKWKGTRPKPLEYVVDNAQGDSDLKLN 360  
 Db 301 VPPTNLSLYCLAPESA PCDGVGSADGSP1KVTKWKGTRPKPLEYVVDNAQGDSDLKLN 360

Qy 361 WTRLPGNLSLTLPGFEGKGGPYRITVTAVSGGLAAAPSWSWGFRRELVPLAGPAWRLP 420  
 Db 361 WTRLPGNLSLTLPGFEGKGGPYRITVTAVSGGLAAAPSWSWGFRRELVPLAGPAWRLP 420

Qy 421 DDPGPtpVVAAGEVPHOLRQATHTFC1QSRGLSTCVNNSSTOTATLPNLHGSFK 480  
 Db 421 DDPGPtpVVAAGEVPHOLRQATHTFC1QSRGLSTCVNNSSTOTATLPNLHGSFK 480

Qy 481 LWVTVSTVAGGPPGPDLSLHLPDRNIRKALLPNFSLNLGCGLSIASTRCLQARC 540  
 Db 481 LWVTVSTVAGGPPGPDLSLHLPDRNIRKALLPNFSLNLGCGLSIASTRCLQARC 540

Qy 541 LHWRHKLLPOWIWVVPDPANSNSCQYIKEVSLPQPKDPILEVEELQPVVESPKA 600  
 Db 541 LHWRHKLLPOWIWVVPDPANSNSCQYIKEVSLPQPKDPILEVEELQPVVESPKA 600

Db 541 LHWRHKLLPOWIWVVPDPANSNSCQYIKEVSLPQPKDPILEVEELQPVVESPKA 600  
 Qy 601 SAPIYSYEKHFELPTPEELGLV 623  
 Db 601 SAPIYSYEKHFELPTPEELGLV 623

RESULT 4  
 US-08-653-740-5  
 ; Sequence 5, Application US/08653740-5  
 ; Patent No. 5792850  
 ; GENERAL INFORMATION:  
 ; APPLICANT: James W. Baumgartner  
 ; APPLICANT: Donald C. Fosser  
 ; APPLICANT: Frank J. Grant  
 ; APPLICANT: Cindy A. Sprecher  
 ; TITLE OF INVENTION: HEMATOPOETIC CYTOKINE RECEPTOR  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: ZymoGenetics, Inc.  
 ; STREET: 1201 Eastlake Avenue East  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/653,740  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Parker, Gary E  
 ; REGISTRATION NUMBER: 31,648  
 ; PREFERENCE/DOCKET NUMBER: 95-31  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 206-442-6673  
 ; TELEFAX: 206-442-6678  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 636 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

US-08-653-740-5

Query Match 59.7%; Score 2044; DB 1; Length 636;  
 Best Local Similarity 62.8%; Pred. No. 4.4e-171;  
 Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

Qy 9 LTPLELLSMLSLIGTRPHGSPGLCYSVPLGILNCSWEPGLDLETTPVLYHOSQK 68  
 Db 14 LPKLAUPLLNLFQTRPQSAGQCYGVGLDNLNCWSBPLGDAPEBLHQSQK 73

Qy 69 HPNRWVEVKPSKOSHNTTIPREQFTMADKLJLWGTGRPLMSVNLLETQMPDPQI 128  
 Db 74 RSNKTOTAVAAGRSMVAIPREQLTMSDKLJLWGTKGAPLWPPYEVNLLETQMKPNAPRL 133

Qy 129 FSQVDISEATLAEATVQAPPWPPQKALTCQFRYKECQAEMWTRLEPQLKTIPLTPEV 188  
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Qy 189 QNLPGTQYGSRCOENGYPGEWSSPLSFOTPLDPDWGSTVCETS GKRALL 247  
 Db 194 QDLELATGKYGRCMKEEDLWGWSPUSFOTPSAPDWWGNLQGFBEPPLL 253

Qy 248 WKDPRPCVQVTTWFAAGDTTQEIVPCCSKSPVAMENAVSPNSTWYPPNTL'S 307  
 Db 254 LWKAPSPCQVSYKTMFWVGRELSPGTCVCCSLIPSGAEWARSAVNTSWEDLNL'S 313

RESULT 5

; Sequence 5 Application US/09073594  
; Patent No. 592535  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; ZIP: 98102

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; APPLICATION NUMBER: US/09/073,594  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-073-594-5

Query Match 59.7% Score 2044; DB 2; Length 636;  
Best Local Similarity 62.8%; Pred. No. 4.4e-171; Indels 8; Gaps 3;

QY 308 LVCLAPESAPCDVGSSADSP3IKYTWKQGTRKPLEVYVDIAQGDSDLKUNWTRLPPG 367  
Db 314 LWCLDSASAPRSVAVSSTAGS3TLLVWQPGGEPELEHVVWDKWARDGPLEKLNWVRLLPPG 373  
QY 368 NLSTLPGPGEFKGSVPYRITVAVSGGLAAAPSWSMGFREELYPLGAFAWRLLPDDPGTP 427  
Db 374 NLSSLALPONFTVGPYRITVAVASGLASSVWGFREELPLVGPFLWRIQDAPPGT 433  
QY 428 YAWGEYPRHQJRGQATHYTFCTQSRGSTYCRNVSQOTATLPNLHSGSKLWVYST 487  
Db 434 ATAWGEYPRHQJRGHLTHYLQRQSGTSRPSVYNSVNTQSFLDPWGPBLWVTAAT 493  
QY 488 VAGQGPPEPDLSLHLDPNRIRKALPAFLSLAGLMMCGLSSLASTRCQARCLHWRHKL 547  
Db 494 IACQGPPPEPILRLHPDNTLWRKVLPGFLFLGFLIGCGLSSLATS ---GRCYHLRKV 549  
QY 548 LIPOMIWERVPDANSNSQPYKEVSLFQPDRGPIDLEVEEYELQPVVES --PKASAPI 604  
Db 550 LPRWWVKEVDPDANSQSSQPHMEQVPEAQPLGDLPILEVEEMEPYPMESSQPAQTAPL 609  
QY 605 YSYEKIFLPTPEELGLL 622  
Db 610 DSGYEKHFPLTPEELGLL 627

QY 9 LTPLELLLSMLLIGTRPHGSPGPLQCYSVGPGCILNCSEPLGDLTEPPVLYHOSQKY 68  
Db 14 LPKLAUPLLWAVLFLORTPOGSAQPLQCYGPGDQNLNCSEPLGDLGAPSELHQSQKY 73  
QY 69 HPNRVWEVKVPSKOSWVTPREQFTMADKLITWGTOKGRLWMSVSVNLETOMKPDTPQI 128  
Db 74 RSNKTQTVAVAAGRSMVATPAREQLTNSDKLWVGTAGQPLWPVNVNLETQMKPNAQL 133  
QY 129 FSQDVISEATLEATYQWAPPWPPQKALTQFRYKECQABAATRLEPLQKLTGJTPVEM 188  
Db 134 GDPVDFSEDDPLEATWVAPPWPSHKVLLICOFHYRCQEAATLLEPELKTIPLTPVEI 193  
QY 189 QNLEPGTCYQVSGRQCQVENGYP-WGENSPSLSFOTPLDPEDWVSGTVCETSGKRAALL 247  
Db 194 QDLELATGKYKYGRCRMKEEDLGWSPMSFOTPSAPDQWVSGNLCSTPGGEBPLL 253  
QY 248 VWKDPKRPCQVQTYTWNGAGDTTTOBEPCKSPVPAWMERAVVSPGNSTSWSWPPTNLS 307  
Db 254 LWKAPGCVQSYKVNFWVGGRRELSPSEGTTCCSLIPSGBEWARYSAVNATSWEPLTNLS 313  
QY 308 LVCLAPESAPCDVGSSADSPGKIVTWQGTRKPLEYVWDQDGSDSLKLNWTRLPPG 367  
Db 314 LVCLDSASAPRSVAVSIIAGSTELLVWQGPGLPELHVWDARDGDPLEKLNWTRLPPG 373  
QY 368 NLSTLPGEFKGVPYRITVAVSGGLAAAPSWSMGFREELYPLGAFAWRLLPDDPGTP 427  
Db 374 NLSSLALPONFTVGPYRITVAVASGLASSVWGFREELPLVGPFLWRIQDAPPGT 433  
QY 428 VVAGGEYPRHQJRGQATHYTFCTQSRGSTYCRNVSQOTATLPNLHSGSKFKLWVYST 487  
Db 434 AIAGGEYPRHQJRGHLTHYLQRQSGTSRPSVCMNSGNTQSFLDPWGPCELMVTAAT 493  
QY 488 VAGQGPPEPDLSLHLDPNRIRKALPAFLSLAGLMMCGLSSLASTRCQARCLHWRHKL 547  
Db 494 IAGQGPPEPILRLHPDNTLWRKVLPGFLFLGFLIGCGLSSLATS ---GRCYHLRKV 549  
QY 548 LFQWIWERVPDANSNSQPYKEVSLFQPDRGPIDLEVEEYELQPVVES --PKASAPI 604  
Db 550 LPRWWVKEVDPDANSQSSQPHMEQVPEAQPLGDLPILEVEEMEPYPMESSQPAQTAPL 609  
QY 605 YSGYEKHFPLTPEELGLL 622  
Db 610 DSGYEKHFPLTPEELGLL 627

RESULT 6

US-09-275-525-5

; Sequence 5 Application US/09275925  
; Sequence 5, Application US/09275925  
; Patent No. 6080406  
; GENERAL INFORMATION:  
; APPLICANT: James W. Baumgartner  
; APPLICANT: Donald C. Foster  
; APPLICANT: Frank J. Grant  
; APPLICANT: Cindy A. Sprecher  
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; APPLICATION NUMBER: US/09/073,594  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31,648  
; REFERENCE/DOCKET NUMBER: 95-31  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6673  
; TELEFAX: 206-442-6678  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 636 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; CURRENT APPLICATION DATA:  
; Query Match 59.7% Score 2044; DB 2; Length 636;  
; Best Local Similarity 62.8%; Pred. No. 4.4e-171; Indels 8; Gaps 3;

NAME: Parker, Gary E  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 636 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
-09-275-925-5

NAME: Parker, Gary E  
 REGISTRATION NUMBER: 31,648  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 636 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -09-275-225-5

Query Match 59.7%; Score 2044; DB 3; Length 636;  
 Best Local Similarity 62.8%; Pred. No. 4.4e-171;  
 Matches 388; Conservative 61; Mismatches 161; Indels 8; Gaps 3;

9 LPLELLSLSMSLLGTRPHGSPPGLQCYSGVPLGTNCNSWEPGLDLETPPVLYHQSQKY 68  
 14 LPKLALLPMLNVLQFQTRPGASQPLQCYGVGPDGLNCNSWEPGLDQGAPSELHQSQY 73

69 HPNRWEVKPSKQSHVTPPEQFTMDKLJLWQGRKQPMWSSVNLQTMKPTPQI 128  
 74 RSNKTQTVAGRSWVAIPREQLTMSDKLWVGTAKQPIWPYFVNLTQMKPNAPRL 133

129 FSQVDISEEATLEATQWAQFWPPQPKALTQFRYKECQEAWTLEPQLTKDTGLTPVEM 188  
 134 GPDVDESEDDPDEATVHWAQFWPPSKVLIQCFHYRCQEAWTLEPELKTIPTPVEI 193  
 189 QNLPGTCYQVSQRCQVENGYP-WGEWSPSLSFQTFPFLPEDWWSGTVCETSGKRAALL 247  
 194 QDLELATQYKVGRCRMEKEEDLNGEWSPLSFQTPPSAKRDWVNSGNLCTGPGEPEPLL 253

248 VWDKDPCPCVOTYTWWFGAGDTTQEYEVCPKSKPSQPAWVSPGNSTSWPPNTLS 307  
 254 LWKAGPQCVQSYKTFWWVGRELSPGEGITCCSLLPSAFAWRAYSAVNTSWEPITNL 313

308 LVCLAPESAPDGVSADGSPGIKVWKGOKTTRKPLEYYWDWAQDSDLUKLNTRFLPPG 367  
 314 LVCLDOSASAPSVAVSSIAGSTELLYTWQGPGEPEHVDWARDGDPLEXLNWRLLPPG 373

368 NLSTLLPGEFKGGPYRITYTAVYSGGLAAAPSYNGFREELVPLAGPAVWRLPDPPGTP 427  
 374 NLSALLPQGNTVGPYRITYTAVASGLASASVSYNGFREELVPLGVTWRLQDAPPGTP 433

428 VAWGEPYPRDQRGQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST 487  
 434 AIWAEVGPYPRDQRGHUYTHLCAQSGTSPSVCMNYSGNTQSVTLPDWGPCELWYTA 493

488 VAGQGPPGPDLSLHLDPNRTRKWLPAFLWFLSMLGILMGCGLSLASSTRCLOARCLWRHKL 547  
 494 IAGQQGPPGPILRFLHLDNTLRKWLPAFLWFLGILGCGLISLATS----GRCHIRHKV 549

548 LPQWMTWERVPDPANSNSGQYIKEYSLPQPKDGTLEVEEVELOPYES - -PKASAPI 604  
 550 LPRWYMEKVPDPANSSSGQMEQYPEAQPLGDLPLEVEEMPPVMMESSQPAQATPL 609

605 YSGYERHFLPTEPEELLL 622  
 610 DSGYERHFLPTEPEELLL 627

RESULT 7  
 -08-653-740-3  
 Sequence 3, Application US/08653740  
 Patent No. 5792850  
 GENERAL INFORMATION:  
 APPLICANT: James W. Baumgartner  
 APPLICANT: Donald C. Foster  
 APPLICANT: Frank J. Grant  
 APPLICANT: Cindy A. Spracher  
 APPLICANT: TAGOG PEP TIGHT POINT PARKYI PCTLFLNGTFLIGCGLSLASTRC  
 TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/653,740  
 FILING DATE: 08/08/2001  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parker, GTY E  
 REGISTRATION NUMBER: 31,648  
 REFERENCE/DOCKET NUMBER: 95-311  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6673  
 TELEFAX: 206-442-6678  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 578 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-653-740-3

Query	Match	Score	DB	Best Local Similarity	Local Similarity	Matches	Conservative	Mismatches	Indel	Length	Type
Qy	9	54.5%	HPNRWEVKPSKQSHVTPPEQFTMDKLJLWQGRKQPMWSSVNLQTMKPTPQI	61.7%	Pred. No. 1.e-155	9	LPLELLSLSMSLLGTRPHGSPPGLQCYSGVPLGTNCNSWEPGLDQGAPSELHQSQY	61.7%	3	636	Linear
Qy	14	54.5%	LPKLALLPMLNVLQFQTRPGASQPLQCYGVGPDGLNCNSWEPGLDQGAPSELHQSQY	61.7%	Pred. No. 1.e-155	14	LPKLALLPMLNVLQFQTRPGASQPLQCYGVGPDGLNCNSWEPGLDQGAPSELHQSQY	61.7%	3	636	Linear
Qy	69	54.5%	HPNRWEVKPSKQSHVTPPEQFTMDKLJLWQGRKQPMWSSVNLQTMKPTPQI	61.7%	Pred. No. 1.e-155	69	HPNRWEVKPSKQSHVTPPEQFTMDKLJLWQGRKQPMWSSVNLQTMKPTPQI	61.7%	3	636	Linear
Qy	74	54.5%	RSNKTOVTAVAGRSWVAIPREQLTMSDKLWVGTAKQPIWPYFVNLTQMKPNAPRL	61.7%	Pred. No. 1.e-155	74	RSNKTOVTAVAGRSWVAIPREQLTMSDKLWVGTAKQPIWPYFVNLTQMKPNAPRL	61.7%	3	636	Linear
Qy	129	54.5%	FSQVDISEEATLEATQWAQFWPPQPKALTQFRYKECQEAWTLEPQLTKDTGLTPVEM	61.7%	Pred. No. 1.e-155	129	FSQVDISEEATLEATQWAQFWPPQPKALTQFRYKECQEAWTLEPQLTKDTGLTPVEM	61.7%	3	636	Linear
Qy	134	54.5%	GPDVDESEDDPDEATVHWAQFWPPSKVLIQCFHYRCQEAWTLEPELKTIPTPVEI	61.7%	Pred. No. 1.e-155	134	GPDVDESEDDPDEATVHWAQFWPPSKVLIQCFHYRCQEAWTLEPELKTIPTPVEI	61.7%	3	636	Linear
Qy	189	54.5%	QNLPGTCYQVSQRCQVENGYP-WGEWSPSLSFQTFPFLPEDWWSGTVCETSGKRAALL	61.7%	Pred. No. 1.e-155	189	QNLPGTCYQVSQRCQVENGYP-WGEWSPSLSFQTFPFLPEDWWSGTVCETSGKRAALL	61.7%	3	636	Linear
Qy	194	54.5%	QDLELATQYKVGRCRMEKEEDLNGEWSPLSFQTPPSAKRDWVNSGNLCTGPGEPEPLL	61.7%	Pred. No. 1.e-155	194	QDLELATQYKVGRCRMEKEEDLNGEWSPLSFQTPPSAKRDWVNSGNLCTGPGEPEPLL	61.7%	3	636	Linear
Qy	248	54.5%	VWDKDPCPCVOTYTWWFGAGDTTQEYEVCPKSKPSQPAWVSPGNSTSWPPNTLS	61.7%	Pred. No. 1.e-155	248	VWDKDPCPCVOTYTWWFGAGDTTQEYEVCPKSKPSQPAWVSPGNSTSWPPNTLS	61.7%	3	636	Linear
Qy	254	54.5%	LWKAGPQCVQSYKTFWWVGRELSPGEGITCCSLLPSAFAWRAYSAVNTSWEPITNL	61.7%	Pred. No. 1.e-155	254	LWKAGPQCVQSYKTFWWVGRELSPGEGITCCSLLPSAFAWRAYSAVNTSWEPITNL	61.7%	3	636	Linear
Qy	308	54.5%	LVCLAPESAPDGVSADGSPGIKVWKGOKTTRKPLEYYWDWAQDSDLUKLNTRFLPPG	61.7%	Pred. No. 1.e-155	308	LVCLAPESAPDGVSADGSPGIKVWKGOKTTRKPLEYYWDWAQDSDLUKLNTRFLPPG	61.7%	3	636	Linear
Qy	314	54.5%	LVCLDOSASAPSVAVSSIAGSTELLYTWQGPGEPEHVDWARDGDPLEXLNWRLLPPG	61.7%	Pred. No. 1.e-155	314	LVCLDOSASAPSVAVSSIAGSTELLYTWQGPGEPEHVDWARDGDPLEXLNWRLLPPG	61.7%	3	636	Linear
Qy	368	54.5%	NLSTLLPGEFKGGPYRITYTAVYSGGLAAAPSYNGFREELVPLAGPAVWRLPDPPGTP	61.7%	Pred. No. 1.e-155	368	NLSTLLPGEFKGGPYRITYTAVYSGGLAAAPSYNGFREELVPLAGPAVWRLPDPPGTP	61.7%	3	636	Linear
Qy	374	54.5%	NLSALLPQGNTVGPYRITYTAVASGLASASVSYNGFREELVPLGVTWRLQDAPPGTP	61.7%	Pred. No. 1.e-155	374	NLSALLPQGNTVGPYRITYTAVASGLASASVSYNGFREELVPLGVTWRLQDAPPGTP	61.7%	3	636	Linear
Qy	428	54.5%	VAWGEPYPRDQRGQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST	61.7%	Pred. No. 1.e-155	428	VAWGEPYPRDQRGQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST	61.7%	3	636	Linear
Qy	434	54.5%	AIWAEVGPYPRDQRGHUYTHLCAQSGTSPSVCMNYSGNTQSVTLPDWGPCELWYTA	61.7%	Pred. No. 1.e-155	434	AIWAEVGPYPRDQRGHUYTHLCAQSGTSPSVCMNYSGNTQSVTLPDWGPCELWYTA	61.7%	3	636	Linear
Qy	488	54.5%	VAGQGPPGPDLSLHLDPNRTRKWLPAFLWFLSMLGILMGCGLSLASSTRCLOARCLWRHKL	61.7%	Pred. No. 1.e-155	488	VAGQGPPGPDLSLHLDPNRTRKWLPAFLWFLSMLGILMGCGLSLASSTRCLOARCLWRHKL	61.7%	3	636	Linear
Qy	494	54.5%	IAGQQGPPGPILRFLHLDNTLRKWLPAFLWFLGILGCGLISLATS----GRCHIRHKV	61.7%	Pred. No. 1.e-155	494	IAGQQGPPGPILRFLHLDNTLRKWLPAFLWFLGILGCGLISLATS----GRCHIRHKV	61.7%	3	636	Linear
Qy	548	54.5%	LPQWMTWERVPDPANSNSGQYIKEYSLPQPKDGTLEVEEVELOPYES - -PKASAPI	604	Pred. No. 1.e-155	548	LPQWMTWERVPDPANSNSGQYIKEYSLPQPKDGTLEVEEVELOPYES - -PKASAPI	604	3	636	Linear
Qy	550	54.5%	LPRWYMEKVPDPANSSSGQMEQYPEAQPLGDLPLEVEEMPPVMMESSQPAQATPL	609	Pred. No. 1.e-155	550	LPRWYMEKVPDPANSSSGQMEQYPEAQPLGDLPLEVEEMPPVMMESSQPAQATPL	609	3	636	Linear
Qy	605	54.5%	YSGYERHFLPTEPEELLL 622			605	YSGYERHFLPTEPEELLL 622		3	636	Linear
Qy	610	54.5%	DSGYERHFLPTEPEELLL 627			610	DSGYERHFLPTEPEELLL 627		3	636	Linear
Qy	374	54.5%	NLSALLEPQGNTVGPYRITYTAVASGLASASVSYNGFREELVPLGVTWRLQDAPPGTP	61.7%	Pred. No. 1.e-155	374	NLSALLEPQGNTVGPYRITYTAVASGLASASVSYNGFREELVPLGVTWRLQDAPPGTP	61.7%	3	636	Linear
Qy	428	54.5%	VVAGGEVPRHQLRQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST	61.7%	Pred. No. 1.e-155	428	VVAGGEVPRHQLRQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST	61.7%	3	636	Linear
Qy	434	54.5%	AIWAGEVPRHQLRQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST	61.7%	Pred. No. 1.e-155	434	AIWAGEVPRHQLRQATHYFCIQSGLSIVCRNYSQQTATLNLHSCEFLMVTST	61.7%	3	636	Linear
Qy	488	54.5%	VAGQGPPGPDLSLHLDPNRTRKWLPAFLWFLSMLGILMGCGLSLASSTRCLOARCLWRHKL	61.7%	Pred. No. 1.e-155	488	VAGQGPPGPDLSLHLDPNRTRKWLPAFLWFLSMLGILMGCGLSLASSTRCLOARCLWRHKL	61.7%	3	636	Linear
Qy	494	54.5%	TAGOG PEP TIGHT POINT PARKYI PCTLFLNGTFLIGCGLSLASTRC	61.7%	Pred. No. 1.e-155	494	TAGOG PEP TIGHT POINT PARKYI PCTLFLNGTFLIGCGLSLASTRC	61.7%	3	636	Linear



RESULT 10  
 US-08-685-118-2  
 ; Sequence 2, Application US/08685118  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gubler, Ulrich A  
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/685,118  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Silverman, Robert A  
 ; REFERENCE/DOCKET NUMBER: 35, 682  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201) 235-2863  
 ; TELEFAX: (201) 235-2363  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 862 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear

MOLECULE TYPE: protein  
 US-08-685-118-2

---

Db 74 RSNKQTQVAVAGRSWAATPREQLTMSDKLUVWGTAKAGPQFLPPVFVNLETQMKNAPRL 133  
 Qy 129 FSOVDTSEEAATLETYQWAPPVNPQPKAATCQFYKECAEAATRLEPQKTDGUTPYEM 188  
 Db 134 GDPVDESDPDLLEATVHWRPSPHKVQIHYRCOBAATLLEPEKTIPLTPVII 193  
 Qy 189 QNLERGTCTYQVSGRCQVENGYP-MGEWSSPLSFQTFPLDPEWVSGTCVETSGSKRAALL 247  
 Db 194 QDLELATGKVYGRMRMEKEEDLNGEWSPLSFQTPPSAPKDIWVSGNLCGTPGEEPL 253  
 Qy 248 VWDPRPCVQVTTVWFGAGDITPQEVEVPCCKSPVPAWMEAWVSPGNISTSWVPPTNLS 307  
 Db 254 LWKAPGCPYQSYKWFNWYGGRELSPGEGTCCLSLIPSGAEWARVSAVNTSWEPLTNLS 313  
 Qy 308 LVCALAPESACPDVCEVSADSPGIGKTVWKGTRPELEYVWDAQDGDSUDKLAKNTRLPFG 367  
 Db 314 LVCLDASAPRSVASSIASTGSELLTVWQGPGELEHVWDADGDPLBLKANVRLPFG 373  
 Qv [REDACTED] NLSTLLPGBEFKGGPYRITVYVSSGLAAAPSPWGFREELVPLAGPAWRLPDDPGTP 427  
 Db 374 NLSALLPGNFTVGPYRITVYAVASGLASSYSGFREELAPLVGPTLWRLQDAPPCTP 433  
 Qy 428 VVANGEVPRHQLRGOATHYFTCIGSLGSTCRVNSSQQTATPLNLSGSFKLUWTVST 487  
 Db 434 AIANGEVPRHQRLGHLTHTLCAQSQTSPSCVMVSGNTQSTLPDLPNGPCELWVAST 493  
 Qy 488 VAGOPPGPDPDLSLHPDNRIWKALPWFSLWGLGILMGGSLASTRCIQRACHWREKL 547  
 Db 494 IAGOPPGPDTLRLHPDNTRLWKVLPGLFLWGFLLGCGSLATS---GRCYHLHRKV 549  
 Qy 548 LPQNTWERYVPDANSNSGQPYIKEVSLPQPQPK 579  
 Db 550 LPRNWWERVPDANSSSG---LIGSPPR 573

RESULT 11  
 US-08-685-118-2  
 ; Sequence 2, Application US/08685118  
 ; Patent No. 6850530  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presky, David H  
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/685,118  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Silverman, Robert A  
 ; REFERENCE/DOCKET NUMBER: CD 9195  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201) 235-2863  
 ; TELEFAX: (201) 235-2363  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 862 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear

Query Match 5 RVARLTPLLEUJLSMSLJLUGTRPHGSPGPLOCYSVGPGLGILNCSWEPPLGD-LETPPVLY 62  
 Best Local Similarity 88; Pred. No. 3.8e-25;  
 Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;  
 Db 102 KLACINSDEIQIGAEIIFYGVAPE-QPNLUSCIONGEQIVACIWGRGRTHLTEYTLQ 160  
 Qy 63 HQSKQYHPNRYWEVK-----VPSKSWVTIPREQFTMAKDLINGTQKGR 107  
 Db 161 LSGPK-NUTWOKOCKDITYCDYDGLDFGINLTPE-----PESNNTAKYTAV-----N 204  
 Qy 108 PLWSSVSVNLETQMKPDTQPIQSQVDISEATLEATVQWAPPVWPP-QKA-----156  
 Db 205 SLGSSSSL-----PSTETFELD-----VPRLPP-WDIRIKFQKASVRCCTL 244  
 Qy 157 -----LTCQFRYKECQEAWTLEPQLKTGDGTPEMVONLEPGTCY-QVSGRCQVE 206  
 Db 245 YWRDEGLVLNLNRVPSNSRLNNNNV--VTAKAGRHDLLDKPTEYEFOISSKLHLY 301  
 Qy 207 NGYPGEWSSPLSFQTPFLDPE-DWVSSGTVCETSGKRAALLWKK-----DPRPCV-- 256  
 Db 302 KG-SWSDWBSLRLATCPEEBTGMIDWVNMKRHIYSROTSLSFWKLNLSVSEARGKILH 359  
 Qy 257 -QVTTWFWFAGDITTTQEVPCCKSPVPMMEAV-VSGNNTSWPPPTNLS--VCLA 312  
 Db 360 YQVTLQELTGKAMTONITGHTSMNTVTPGTGNWAVAVSAANSKGSSLPRINMINACEA 419  
 Qy 313 PESAPCDVGSSADSPGIVKTVWKGTRKP--LEYVWDRAQ--DGDSLQKLWTRLPP 366  
 Db 420 GLLAPRQVSANS-EGMDNILTVTWPQPRDBSAVQEVYVERELHGGDQVPLWLRSRP 478  
 Qy 367 GNLSTLPGFEGKGGPYRITVYVSGGLAAAPSPWGFREELVPLAGPAWRLPDDPGTP 426  
 Db 479 YNVSAJISENIKSYCIEIRYVAL-SGDOGCSLTLGNSKHKAPUSPHNATIYEE-KGS 536  
 Qy 427 PVVANGEVPRHQLRGOATHYFTCIGSLGSTVCRVNSQQTATPLV-----NLH-----475  
 Db 537 ILISNSNIPYQEONGCLHYRIWKE-----RDNSQPOLCEPYRSQNOSHPINSLQ 589  
 Qy 476 -SGSEKLAWTVSTVAGQGPDPDLSLHPPDRNIRWKALPFLSLWGLLNGCGUSLASTR 534  
 Db 590 PRVIVYLWATLTAEGSSHIGNEREFCL-OQKANWMAFVAPSICIAINVG---IFSPH 644  
 Qy 535 CLOARCLHWKHLPKQWVWVPRDPANSNSGQPYIKEVSLPQPQPK-----PKDGP1 583  
 Db 645 YFOQQKVFWILLAALRQWMSREIPDANSICAKKVIPIAEKTKQLPDRLLDWMPPEPDPEP 704

RESULT 11  
 US-08-915-495-2  
 ; Sequence 2, Application US/08915495  
 ; Patent No. 5852176  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gubler, Ulrich A  
 ; TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/685,118  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Silverman, Robert A  
 ; REFERENCE/DOCKET NUMBER: 35, 682  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201) 235-2863  
 ; TELEFAX: (201) 235-2363  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 862 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/915,495  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/605,118  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silverman, Robert A.  
 REGISTRATION NUMBER: 35,682  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 235-2853  
 TELEX/FAX: (201) 235-2363  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 862 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-915-495-2

Query Match 11.28; Score 384; DB 2; Length 862;  
 Best Local Similarity 25.1%; Pred. No. 3.8e-25;  
 Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

Qy 5 RYARLPLELLSLSMULLGTRPHGSPGPLQCYSVGPLGINCSWPLGLD--LETPPVLY 62  
 Db 102 KLAICNSDEIQCGAEIFVGIAPE-QFQNLSLQHQEQGTVACTWERGDTLYTEYTQ 160  
 Qy 63 HQSQKYPNRYBVK-----VPSKQSWVVTIPREQTMADKLJWGTQKGR 107  
 Db 161 LSGPK--NLWIKQOCKDIYCDYLDGFINLTPE-----PESNTAKVTAV-----N 204  
 Qy 108 PLASSVSYNLIEQMKPDTPQITSDVQDISEATLEATYQWAPPWPP----OKA-----156  
 Db 205 SGSSSSS-----PSTFLD-----VRPLP-WDIRIKFORASYSRCTL 244  
 Qy 157 -----LTCOFRYKECQAFAPWTRLEPQLKTDPVEMONLERSTCY---QVSGRQCVE 206  
 Db 245 YWRDEGLYLNRLNRYRPSNSRNHYMN--VTKAKGRHDLDDLKPTTEYEFQISSKLHY 301  
 Qy 207 NGYPWGNESSPSPSFOPPFDPB---DVWVSGTVCETSGKRALLYWK-----DPRPCV-- 256  
 Db 302 KG-SWSWSESESRAQIPEEEPTGMLDWYMKRHDYSRQISLF-WKNLVSSEARGKILH 359  
 Qy 257 -OVTYTWFEGACDITTTQEEYPCCKSPVPAWWAY-VSPGNSTSIVPPTNSL--VCLA 312  
 Db 360 YOTLQBLLTGKAMTONITGHTSWTWIVIPRTGIVAWASAANSKGSSLPRININNLCEA 419  
 Qy 313 PESAPCDGVSSADGSPGIKVTKQGTRKP--LEYVDDNAQ---DGDSLKLNWTRLPP 366  
 Db 420 GLIAPROVANS-EGMDNLYWLWOPRKDPSAVQEYVVENRELHPGDTQVPLNWLRSRP 478  
 Qy 367 GNISTLPGFEGGGVPYRITYAVSGGLAAPSPWGFREELVPLAGPATWRLPDDPPGT 426  
 Db 479 YNVALSLENKSYCIEIRYAL-SGDOGCCSILGNSKHKAPLSGHFINATEB-KGS 536  
 Qy 427 PVVAWGEVPRHOLRGQATHYTCIQSRLSTVCRNVSQTOATLP-----NLH-----475  
 Db 537 ILISWNSIPVQBMGCLLHYRYWKE----RDNSNQPOLCEPYRVSONSHPINSLQ 589  
 Qy 476 -SGSFKLWVTVAGQGPPGFDLSLHLPDNRIRKALPFLSLNGLLNGCGLSLASTR 534  
 Db 530 PRVTVWMMTAATAEGSSHNEFCL-OCKANMNAFAVAPSICIAIMVG----IFSTH 644  
 Qy 535 CLQARCLHWRHKLLPWIWERYVDPANSNSQQPY-IKEVSLQP-----PKDGP 583

RESULT 12  
 US-08-914-520-2  
 Sequence 2, Application US/08914520  
 Patent No. 5919903  
 GENERAL INFORMATION:  
 APPLICANT: Gubler, Ulrich A  
 PRESKY, David H  
 TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 07110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/914,520  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY DOCKET NUMBER: CD 9195  
 APPLICATION NUMBER: 08/685,118  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silverman, Robert A.  
 REGISTRATION NUMBER: 35,682  
 REFERENCE/DOCKET NUMBER: CD 9195  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 235-2863  
 TELEFAX: (201) 235-2363  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 862 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-914-520-2

Query Match 11.28; Score 384; DB 2; Length 862;  
 Best Local Similarity 25.1%; Pred. No. 3.8e-25;  
 Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

Qy 5 RVARLPLELLSLSMULLGTRPHGSPGPLQCYSVGPLGINCSWPLGLD--LETPPVLY 62  
 Db 102 KLAICNSDEIQCGAEIFVGIAPE-QFQNLSLQHQEQGTVACTWERGDTLYTEYTQ 160  
 Qy 63 HQSQKYPNRYBVK-----VPSKQSWVVTIPREQTMADKLJWGTQKGR 107  
 Db 161 LSGPK--NLWIKQOCKDIYCDYLDGFINLTPE-----PESNTAKVTAV-----N 204  
 Qy 108 PLASSVSYNLIEQMKPDTPQITSDVQDISEATLEATYQWAPPWPP----OKA-----156  
 Db 205 SGSSSSS-----PSTFLD-----VRPLP-WDIRIKFORASYSRCTL 244  
 Qy 157 -----LTCOFRYKECQAFAPWTRLEPQLKTDPVEMONLERSTCY---QVSGRQCVE 206  
 Db 245 YWRDEGLYLNRLNRYRPSNSRNHYMN--VTKAKGRHDLDDLKPTTEYEFQISSKLHY 301  
 Qy 207 NGYPWGNESSPSPSFOPPFDPB---DVWVSGTVCETSGKRALLYWK-----DPRPCV-- 256  
 Db 302 KG-SWSWSESESRAQIPEEEPTGMLDWYMKRHDYSRQISLF-WKNLVSSEARGKILH 359  
 Qy 257 -OVTYTWFEGACDITTTQEEYPCCKSPVPAWWAY-VSPGNSTSIVPPTNSL--VCLA 312  
 Db 360 YOTLQBLLTGKAMTONITGHTSWTWIVIPRTGIVAWASAANSKGSSLPRININNLCEA 419  
 Qy 313 PESAPCDGVSSADGSPGIKVTKQGTRKP--LEYVDDNAQ---DGDSLKLNWTRLPP 366  
 Db 420 GLIAPROVANS-EGMDNLYWLWOPRKDPSAVQEYVVENRELHPGDTQVPLNWLRSRP 478  
 Qy 367 GNISTLPGFEGGGVPYRITYAVSGGLAAPSPWGFREELVPLAGPATWRLPDDPPGT 426  
 Db 479 YNVALSLENKSYCIEIRYAL-SGDOGCCSILGNSKHKAPLSGHFINATEB-KGS 536  
 Qy 427 PVVAWGEVPRHOLRGQATHYTCIQSRLSTVCRNVSQTOATLP-----NLH-----475  
 Db 537 ILISWNSIPVQBMGCLLHYRYWKE----RDNSNQPOLCEPYRVSONSHPINSLQ 589  
 Qy 476 -SGSFKLWVTVAGQGPPGFDLSLHLPDNRIRKALPFLSLNGLLNGCGLSLASTR 534  
 Db 530 PRVTVWMMTAATAEGSSHNEFCL-OCKANMNAFAVAPSICIAIMVG----IFSTH 644  
 Qy 535 CLQARCLHWRHKLLPWIWERYVDPANSNSQQPY-IKEVSLQP-----PKDGP 583

Query Match 11.28; Score 384; DB 2; Length 862;  
 Best Local Similarity 25.1%; Pred. No. 3.8e-25;  
 Matches 171; Conservative 88; Mismatches 281; Indels 140; Gaps 33;

Qy 5 RVARLPLELLSLSMULLGTRPHGSPGPLQCYSVGPLGINCSWPLGLD--LETPPVLY 62  
 Db 102 KLAICNSDEIQCGAEIFVGIAPE-QFQNLSLQHQEQGTVACTWERGDTLYTEYTQ 160  
 Qy 63 HQSQKYPNRYBVK-----VPSKQSWVVTIPREQTMADKLJWGTQKGR 107  
 Db 161 LSGPK--NLWIKQOCKDIYCDYLDGFINLTPE-----PESNTAKVTAV-----N 204  
 Qy 108 PLWSSVSVNLETQMKPDTPQITSDVQDISEATLEATYQWAPPWPP----OKA-----156  
 Db 205 SLGSSSSL-----PSTFLD-----VRPLP-WDIRIKFORASYSRCTL 244  
 Qy 157 -----LTCOFRYKECQAFAPWTRLEPQLKTDPVEMONLERSTCY---QVSGRQCVE 206  
 Db 245 YWRDEGLYLNRLNRYRPSNSRNHYMN--VTKAKGRHDLDDLKPTTEYEFQISSKLHY 301  
 Qy 207 NGYPWGNESSPSPSFOPPFDPB---DVWVSGTVCETSGKRALLYWK-----DPRPCV-- 256  
 Db 302 KG-SWSWSESESRAQIPEEEPTGMLDWYMKRHDYSRQISLF-WKNLVSSEARGKILH 359  
 Qy 257 -OVTYTWFEGACDITTTQEEYPCCKSPVPAWWAY-VSPGNSTSIVPPTNSL--VCLA 312  
 Db 360 YOTLQBLLTGKAMTONITGHTSWTWIVIPRTGIVAWASAANSKGSSLPRININNLCEA 419  
 Qy 313 PESAPCDGVSSADGSPGIKVTKQGTRKP--LEYVDDNAQ---DGDSLKLNWTRLPP 366  
 Db 420 GLIAPROVANS-EGMDNLYWLWOPRKDPSAVQEYVVENRELHPGDTQVPLNWLRSRP 478  
 Qy 367 GNISTLPGFEGGGVPYRITYAVSGGLAAPSPWGFREELVPLAGPATWRLPDDPPGT 426  
 Db 479 YNVALSLENKSYCIEIRYAL-SGDOGCCSILGNSKHKAPLSGHFINATEB-KGS 536  
 Qy 427 PVVAWGEVPRHOLRGQATHYTCIQSRLSTVCRNVSQTOATLP-----NLH-----475  
 Db 537 ILISWNSIPVQBMGCLLHYRYWKE----RDNSNQPOLCEPYRVSONSHPINSLQ 589  
 Qy 476 -SGSFKLWVTVAGQGPPGFDLSLHLPDNRIRKALPFLSLNGLLNGCGLSLASTR 534  
 Db 530 PRVTVWMMTAATAEGSSHNEFCL-OCKANMNAFAVAPSICIAIMVG----IFSTH 644  
 Qy 535 CLQARCLHWRHKLLPWIWERYVDPANSNSQQPY-IKEVSLQP-----PKDGP 583



CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101

COMPUTER READABLE FORM:

COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/797,556  
 FILING DATE: 1991/11/22  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.  
 REGISTRATION NUMBER: 32,172  
 REFERENCE/DOCKET NUMBER: 2607  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-587-0430  
 TELEFAX: 206-587-0606

FORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1001 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-07-797-556-6

---

Query Match 8.18; Score 277; DB 1; Length 1001;  
 Best Local Similarity 21.7%; Pred. No. 1.2e-15;  
 Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

Qy 27 PIGSPGPQCYGPGPGLTLCWEP----LGDLTEPPVYHO-SQKYPNRPNEVKP 79  
 Db 332 PDDTPQQLNC-ETHDLKEICWNPGRVTALVGRATSYTLVESFSKY -VRLRKAEP 388

Oy 80 SKOSW---VTIPREQ---FTMADKLILWGTOKGRPL--WSSVSNLETQMKPDTPQIF 129  
 Db 389 TRESYQLFQMPNQEYNTI-----NAHNPLGRSOSTILVNITERKVYPHTPTSF 439

Oy 130 SQDISEEATLAEATVQHAPPWPPQKALTQFYKECQAEMTRLEPQLTKDGLTP--- 185

Db 440 KVDINSTA---VKSMLPHLPGNFAKINFCLCEIEIKSSNS---VOEQRNVTIKGVNESSYL 493

Oy 186 VENQNLSEGTCTQVSGRQCQVENGPMGEWSLTSRPFLODE--DVWSTGTVCTSGK 242  
 Dp 494 VNLDKLNPTYLTMLFRICSTENFKSKWSNKQKHITTEASPSKGPDWTREWS---SDGK 550

Oy 243 RAALLYWDKPREPCVQ---VYTIVMFAGDTTTOBEVPCCKSKPVPARME----WAVY 292  
 Db 551 N-LIITWK-PFLNEANGKISNSNVCSQSSDETQSLSIEIPPKHAEIRLDKNDYLISSV 608

Oy 293 SPGNSTSWWPPTNLSVUCLAPESAPCDVGYSADG-SPGIKVTTWKOGRTRKPLEYVVDWAQ 351

Db 609 AK-NSSGSSPKIA---SMELPNDDLKTIEQVVMGMKGKILLTWHDPMNTCDYTIKWCN 663

Oy 352 DEDSLDKL-NWRPLPQGNLTLPG-EFKGVFPYRTITAVYSGGLAAAFSVWGPREEV 409

Db 664 SSRSEPCLMDWKRVPNSNTERVIESDEFRPOIYNNFLYGCRRNQGYQLRSMIGYEELA 723

Oy 410 PLAGPAVWRLLPDPGTPVVAWEYVPRHOLRGQATHYTF----CIOSRGLS 456

Db 724 PIVAPN\_FTVETSAISLKVWEDIPVEELRGLFLYFPGKGERDTSMRVLERSRD 782

Oy 457 TWCRNVSQT-TATLPNLH-SGSFLKWLWVTVAGQCPGPDLISHL--PDNRTRWKAL 512

Db 783 IJKVNKTIDISONTLRADLQGKTSYHVLVRAY---DGGVGPKEKSMVYVTKENSY---- 834

Oy 513 PWFLSLWGLL----LMGGGLSLASTRCOARCHWRHLLPOMIWER---VP 557

Db 835 -----GLTIAILIPVAVAVIVGV---VTSILCYRKR-----ENIKEFYPDIP 874

Qy 558 DPANSNS-----GQPIKEVSL-POPPKGDPILE-----VEVE-LQPVVEPSK 599  
 Db 875 NPENCALQFQKSVCGSSAALKTLENPKPNNEVLETRSAFPEKEDTEISPVPAERPE 934

---

RESULT 15  
 US-07-943-843-2  
 ; Sequence 2, Application US/07943843  
 ; Patent No. 5284755

GENERAL INFORMATION:

APPLICANT: Gearing, David P.  
 TITLE OF INVENTION: Leukemia Inhibitory Factor Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/943,843  
 FILING DATE: 1992/09/11  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.  
 REGISTRATION NUMBER: 32,172  
 REFERENCE/DOCKET NUMBER: 2606-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-587-0430  
 TELEFAX: 206-587-0606

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1001 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-07-943-843-2

Query Match 8.1%; Score 277; DB 1; Length 1001;  
 Best Local Similarity 21.7%; Pred. No. 1.2e-15;  
 Matches 143; Conservative 110; Mismatches 263; Indels 144; Gaps 37;

Qy 27 PHGSPGPQCYGPGPGLTLCWEP----LGDLTEPPVYHO-SQKYPNRPNEVKP 79  
 Db 332 PPDTPOQLNC-ETHDLKEICWNPGRVTALVGRATSYTLVESFSKY -VRLRKAEP 388

Oy 80 SKOSW---VTIPREQ---FTMADKLILINGTOKGRPL--WSSVSNLETQMKPDTPQIF 129  
 Db 389 TNEQSLQFLQMLPNOEIYNETL-----NAHNPLGRSOSTILVNITEKVPHTPTSF 439

Qy 130 SQDISEEATLAEATVQHAPPWPPQKALTQFYKECQAEMTRLEPQLTKDGLTP--- 185

Db 440 KVDINSTA---VKSMLPHLPGNFAKINFCLCEIEIKSSNS---VOEQRNVTIKGVNESSYL 493

Qy 186 VENQNLSEGTCTQVSGRQCQVENGPMGEWSLTSRPFLODE--DVWSTGTVCTSGK 242

Db 494 VNLDKLNPTYLTMLFRICSTENFKSKWSNKQKHITTEASPSKGPDWTREWS---SDGK 550

Oy 243 RAALLYWDKPREPCVQ---VYTIVMFAGDTTTOBEVPCCKSKPVPARME----WAVY 292

Db 551 N-LIITWK-PFLNEANGKISNSNVCSQSSDETQSLSIEIPPKHAEIRLDKNDYLISSV 608

Oy 293 SPGNSTSWWPPTNLSVUCLAPESAPCDVGYSADG-SPGIKVTTWKOGRTRKPLEYVVDWAQ 351

Db 609 AK-NSSGSSPKIA---SMELPNDDLKTIEQVVMGMKGKILLTWHDPMNTCDYTIKWCN 663

Qy 352 DEDSLDKL-NWRPLPQGNLTLPG-EFKGVFPYRTITAVYSGGLAAAFSVWGPREEV 409

Db 664 SSRSEPCLMDWKRVPNSNTERVIESDEFRPOIYNNFLYGCRRNQGYQLRSMIGYEELA 723

Oy 410 PLAGPAVWRLLPDPGTPVVAWEYVPRHOLRGQATHYTF----CIOSRGLS 456

Db 724 PIVAPN\_FTVETSAISLKVWEDIPVEELRGLFLYFPGKGERDTSMRVLERSRD 782

Oy 457 TWCRNVSQT-TATLPNLH-SGSFLKWLWVTVAGQCPGPDLISHL--PDNRTRWKAL 512

Db 783 IJKVNKTIDISONTLRADLQGKTSYHVLVRAY---DGGVGPKEKSMVYVTKENSY---- 834

Qy 513 PWFLSLWGLL----LMGGGLSLASTRCOARCHWRHLLPOMIWER---VP 557

Db 835 -----GLTIAILIPVAVAVIVGV---VTSILCYRKR-----ENIKEFYPDIP 874

Qy 558 DPANSNS-----GQPIKEVSL-POPPKGDPILE-----VEVE-LQPVVEPSK 599  
 Db 875 NPENCALQFQKSVCGSSAALKTLENPKPNNEVLETRSAFPEKEDTEISPVPAERPE 934

Oy 352 DGDSDLKL - NWTRLPPGNLSTLLPG - EFKGGVYPRITVTAWSGLAAAPSVMGFREELV 409  
 Db 664 SSRSEPCLMDRKVPSNSTEVIESDEFRPIRYNFFLYCRNQXYQLI<sub>RS</sub>SMIGTYIELA 723  
 Oy 410 PLAGPAWRLDOPPPTPVVAWEYPRHOLQGQATHYF --CITOSRGLS 456  
 Db 724 PIVAPN-FTVBDTSADSILYKWDIPVEELRGFLRGYLFYFGKERDTSKMRVLESGRSD 782  
 Oy 457 TVCRNYSQTO-TATIPNLH SGSPFLWVTVTVAQGQPDPDLSLHL -- PDNRTRWKAL 512  
 Db 783 KVVKNTDISKTKTLRADLOQTKTSHLVRAYT--DGGVPEKSMVVTKENSY----- 834  
 Oy 513 PWFLSLWGLL-----LMGGGLSIALSTRCLQARCLHWRHKLLPQWIER----VP 557  
 Db 835 -----GLIAILIPAVAVIVGV--VTSILCYRKR-----EVTKETYPDIP 874  
 Oy 558 DPANSNS-----GQPYIKEVSL-PQPDKGPILE-----VEEEL-QPVVESPK 599  
 Db 875 NPENCKALQFQKSVCEGSSAALKLEMNPCTPNNEVLETRSAFPKIEDTEISPYAERPE 934

Search completed: May 9, 2002, 06:04:28  
 Job time: 40 sec

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